

SEARCH REQUEST FORM

Scientific and Technical Information Center

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51690

Requester's Full Name: _____ Examiner #: _____ Date: _____
 Art Unit: _____ Phone Number 30 _____ Serial Number: _____
 Mail Box and Bldg/Room Location: _____ Results Format Preferred (circle): PAPER DISK E-MAIL

If more than one search is submitted, please prioritize searches in order of need.

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc, if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: _____

Inventors (please provide full names): _____

Earliest Priority Filing Date: _____

**For Sequence Searches Only* Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.*

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Type of Search		Vendors and cost where applicable
Searcher <u>Toby Fort</u>	NA Sequence (#) <u>1</u>	STN _____
Searcher Phone # <u>308-354</u>	AA Sequence (#) <u>1</u>	Dialog _____
Searcher Location _____	Structure (#) _____	Questel/Tris _____
Date Searcher Picked Up <u>9/26</u>	Bibliographic _____	Dr. Link _____
Date Completed <u>9/28</u>	Litigation _____	Lexis/Nexis _____
Searcher Prep & Review Time <u>10</u>	Fulltext _____	Sequence Systems <u>CS</u>
Clerical Prep Time _____	Patent Family _____	WWW/Internet _____
Online Time <u>10</u>	Other _____	Other (specify) _____

Art : 5/2000

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 26, 2001, 15:15:09 ; Search time 21.33 Seconds
(without alignments)
375.170 Million cell updates/sec

Title: US-09-662-783-4
Perfect score: 737
Sequence: 1 MYLTPRYGRSVHDKSKV.....DIQLDHHRCDCICSSRPPR 132

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 412676 seqs, 60623988 residues

Total number of hits satisfying chosen parameters: 412676

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_0601.*

- 1: /SID88/gcgdata/geneseq/geneseq/AA1980.DAT.*
- 2: /SID88/gcgdata/geneseq/geneseq/AA1981.DAT.*
- 3: /SID88/gcgdata/geneseq/geneseq/AA1982.DAT.*
- 4: /SID88/gcgdata/geneseq/geneseq/AA1983.DAT.*
- 5: /SID88/gcgdata/geneseq/geneseq/AA1984.DAT.*
- 6: /SID88/gcgdata/geneseq/geneseq/AA1985.DAT.*
- 7: /SID88/gcgdata/geneseq/geneseq/AA1986.DAT.*
- 8: /SID88/gcgdata/geneseq/geneseq/AA1987.DAT.*
- 9: /SID88/gcgdata/geneseq/geneseq/AA1988.DAT.*
- 10: /SID88/gcgdata/geneseq/geneseq/AA1989.DAT.*
- 11: /SID88/gcgdata/geneseq/geneseq/AA1990.DAT.*
- 12: /SID88/gcgdata/geneseq/geneseq/AA1991.DAT.*
- 13: /SID88/gcgdata/geneseq/geneseq/AA1992.DAT.*
- 14: /SID88/gcgdata/geneseq/geneseq/AA1993.DAT.*
- 15: /SID88/gcgdata/geneseq/geneseq/AA1994.DAT.*
- 16: /SID88/gcgdata/geneseq/geneseq/AA1995.DAT.*
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- 18: /SID88/gcgdata/geneseq/geneseq/AA1997.DAT.*
- 19: /SID88/gcgdata/geneseq/geneseq/AA1998.DAT.*
- 20: /SID88/gcgdata/geneseq/geneseq/AA1999.DAT.*
- 21: /SID88/gcgdata/geneseq/geneseq/AA2000.DAT.*
- 22: /SID88/gcgdata/geneseq/geneseq/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
5 - 1	737	100.0	322	21	AA1971129 Human Platelet Der
2	737	100.0	370	21	AB48653 Human growth facto
3	737	100.0	370	21	AA198664 SEQ. ID. 37 from W
4 - 4	737	100.0	370	21	AA1971130 Human Platelet Der
5	737	100.0	370	22	AB60888 Human VEGF-G prote
6	713	96.7	200	21	AA1971128 Human Platelet Der
7	686	93.1	370	21	AB48663 Mouse growth facto
8	681	92.4	370	22	AB60895 Human VEGF-G prote
9	380	51.6	66	21	AA1971132 Human Platelet Der
10	330	44.8	374	21	AB10639 Human VEGF-X prote
11	328.5	44.6	149	21	AB10642 Human VEGF-X PDGF-

12	328.5	44.6	318	21	AA194558 A fragment of plat
13	328.5	44.6	339	21	AB58438 Lung cancer associ
14	328.5	44.6	345	20	AA193679 Human VEGF-E prote
15	328.5	44.6	345	20	AA191766 Human PRO200 prote
16	328.5	44.6	345	20	AA190023 Human vascular end
17	328.5	44.6	345	21	AB48657 Human zvegfg3, SEQ
18	328.5	44.6	345	21	AB24250 Human platelet-der
19	328.5	44.6	345	21	AB44322 Human PRO200 (UNQ1
20	328.5	44.6	345	21	AB10633 Human RACE generat
21	328.5	44.6	345	21	AB10634 Human VEGF-X homol
22	328.5	44.6	345	21	AB10635 Human VEGF-X prote
23	328.5	44.6	345	21	AB10636 Human VEGF-X prote
24	328.5	44.6	345	21	AB10644 Human 990126veg p
25	328.5	44.6	345	21	AB10650 Human VEGF-X prote
26	328.5	44.6	345	21	AB10651 Human VEGF-X prote
27	328.5	44.6	345	21	AB19578 Human PRO200 (vasc
28	328.5	44.6	345	21	AB33414 Human PRO200 prote
29	328.5	44.6	345	21	AB24412 Human PRO713 prote
30	328.5	44.6	345	21	AB01419 Human TANGO 128.
31	328.5	44.6	345	21	AB03003 Human growth facto
32	328.5	44.6	345	21	AA196858 Human growth facto
33	328.5	44.6	345	21	AA194557 Amino acid sequenc
34	328.5	44.6	345	21	AA19285 Bone morphogenic p
35	328.5	44.6	345	22	AB50980 Human PRO200 prote
36	328.5	44.6	345	22	AB49895 Human PRO200 prote
37	328.5	44.6	345	22	AB53074 Human angiogenesis
38	324.5	44.0	345	21	AB48658 Mouse zvegfg3, SEQ
39	324.5	44.0	345	21	AA196861 Murine vascular en
40	324.5	44.0	345	21	AA194559 A murine platelet-
41	318.5	43.2	354	21	AB10640 Human VEGF-X prote
42	318.5	43.2	354	21	AB10641 Human VEGF-X prote
43	308.5	41.9	113	21	AB10631 Human VEGF-X prote
44	308.5	41.9	113	21	AB10632 Human VEGF-X prote
45	292	39.6	227	21	AB10637 Human VEGF-X prote

ALIGNMENTS

RESULT 1	
AA1971129	AA1971129 standard; peptide; 322 AA.
ID	AA1971129 standard; peptide; 322 AA.
XX	
AC	AA1971129;
XX	
DF	08-SEP-2000 (first entry)
XX	
DE	Human Platelet Derived Growth Factor (PDGF)-D partial polypeptide #2.
XX	
KW	Platelet Derived Growth Factor-D; PDGF-D; human; cytostatic; vulnerary;
KW	VEGF-G; Vascular Endothelial Growth Factor; antiatherosclerotic; tumour;
KW	proliferative; activator; proliferation; differentiation; motility;
KW	growth; PDGF-D receptor; antagonist; tissue remodelling; treat;
KW	atherosclerosis; wound; metastasis.
OS	Homo sapiens.
XX	
PN	WO200027879-A1.
XX	
PD	18-MAY-2000.
XX	
PF	10-NOV-1999; 99WO-US26462.
XX	
PR	10-NOV-1998; 98US-0107852.
PR	28-DEC-1998; 98US-0113997.
PR	26-AUG-1999; 99US-0150604.
PR	04-OCT-1999; 99US-0157108.
PR	05-OCT-1999; 99US-0157756.
XX	
PA	(LUDW-) LUDWIG INST CANCER RES.
PA	(UYHE-) UNIV HELSINKI LICENSING LTD OY.
XX	
PI	Eriksson U, Aase K, Ponten A, Lee X, Utela M, Alitalo K;

PI Oestman A, Heldin C;
XX WPI: 2000-376495/32.
DR N-PSDB; AAD00737.
XX
XX Novel polynucleotides encoding a novel growth factor of cells
PT expressing a platelet-derived growth factor, useful for diagnostic and
PT therapeutic applications, e.g. concerning cancer -
XX
XX Claim 25; Fig 6; 111pp; English.
XX
CC The present sequence is an N-terminally truncated polypeptide of human
CC platelet derived growth factor (PDGF)-D, formally known as Vascular
CC Endothelial Growth Factor (VEGF)-G. It is derived from human foetal lung
CC Lambda10 cDNA library. It belongs to the VEGF/PDGF family. It functions
CC as an activator of proliferation, differentiation, growth and motility of
CC cells, that express PDGF-D receptor. This sequence is useful for
CC inhibiting the growth of tumours, that express PDGF-D. Expression of
CC PDGF-D and its proteolytic cleavage for generating an activated truncated
CC form is useful for regulating receptor binding specificity of PDGF-D.
CC PDGF-D antagonist is useful for inhibiting tissue remodelling during the
CC invasion of tumour cells into normal cells. PDGF-D may be used to treat
CC wounds, atherosclerosis, metastasis and migration of smooth muscle cells.
XX
XX Sequence 322 AA;
SQ

Query Match 100.0%; Score 737; DB 21; Length 322;
Best Local Similarity 100.0%; Pred No. 1.1e-73;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MYLTPRYGRSYHDKRSKVDLDNDADAKRYSCPTPNYSVNIREEKLANVVFPRCLL 60
Db 191 myldtpyrgsyhdkrskvdlrldndakryscptpnysvniireelkianvffprcll 250

QY 61 VQRCGNCGGTWNRSCTNSCKTVKKYHEVLQFEPGHIKRRGAKTMAVDIQLDHHE 120
Db 251 vqrcgncgcgtwnrsctnscgtkvkkyhevlqfepghikrrgraktmalvdiqlhdhe 310

QY 121 RDCICSSRP 132
Db 311 rdcicssrppr 322

RESULT 2
AAB48653
ID AAB48653 standard; Protein; 370 AA.
XX
XX AAB48653;
XX
XX 09-MAR-2001 (first entry)
DE Human growth factor homologue zveg4, SEQ ID NO:2.
XX
XX Human; zveg4; growth factor homologue; VEGF/PDGF family;
KW CUB domain; PDGF-like activity; mitogenic; osteogenic;
KW neovascularisation; tissue repair; proliferation; differentiation;
KW liver damage; neurodegenerative; Alzheimer's disease; multiple sclerosis;
KW periodontal disease; bone fracture; wound healing; vulnerability; ischaemia;
KW immunomodulation; hepatic; chromosome 11q22.3-23.1.
XX
XX Homo sapiens.
OS
XX
XX WO200066736-A1.
PN
XX
XX 09-NOV-2000.
PD
XX
XX 03-MAY-2000; 2000WO-US40047.
PF
XX
XX 03-MAY-1999; 99US-0304216.
PR
XX 10-NOV-1999; 99US-0164463.
PR
XX 04-FEB-2000; 2000US-0180169.
XX

PA (ZYMO) ZYMOGENETICS INC.
XX
XX Gilbert T, Hart CE, Sheppard PO, Gilbertson DG;
PI
XX WPI: 2000-687541/67.
DR N-PSDB; AAC81555.
XX
XX Growth factor homologs and the nucleic acids that encode them, useful
PT e.g. for treating liver damage, ischemia, multiple sclerosis and
PT Alzheimer's disease -
XX
XX Claim 1; Page 110-111; 143pp; English.
PS
XX The invention relates to the human growth factor homologue zveg4
CC (AAB48653), and nucleic acids encoding it (AAC81555). Zveg4 is a member
CC of the PDGF (platelet-derived growth factor)/VEGF (vascular endothelial
CC growth factor) family. Zveg4 has a growth factor domain (AAB48634)
CC characterised by a PDGF cysteine knot structure, and a CUB domain
CC (AAB48655) which has a beta barrel structure. Zveg4 has PDGF-like
CC activity, having mitogenic activity on fibroblasts, vascular smooth
CC muscle cells and pericytes, and has also been shown to stimulate bone
CC growth. The invention also relates to fusion proteins comprising human
CC zveg4 or fragments thereof, particularly human zveg4/human zveg3
CC fusions; expression constructs and host cells comprising human zveg4
CC nucleic acids; the recombinant expression of human zveg4; an antibody
CC which binds to human zveg4 or a fragment thereof; a method of activating
CC a cell-surface PDGF receptor using a zveg4-derived polypeptide; a
CC method of modulating the proliferation, differentiation, migration or
CC metabolism of bone cells, comprising exposing bone cells to
CC zveg4-derived polypeptides; and a method of detecting a genetic
CC abnormality in the zveg4 gene of a patient. Zveg4 proteins and derived
CC fragments may be used to stimulate tissue development or repair, or
CC cellular differentiation or proliferation. They are particularly used for
CC the treatment or repair of liver damage, and may also be used to
CC modulate neurite growth (e.g., in the treatment of Alzheimer's disease or
CC multiple sclerosis). Due to their osteogenic activity, they may be used
CC in the treatment of periodontal disease and fractures. They may also be
CC used to enhance expansion and mobilisation of haematopoietic stem cells
CC and endothelial precursor stem cells, which may be useful in the
CC treatment of ischaemia, in wound healing, and in the modulation of the
CC immune system. The present sequence represents human zveg4.
XX
XX Sequence 370 AA;
SQ

Query Match 100.0%; Score 737; DB 21; Length 370;
Best Local Similarity 100.0%; Pred No. 1.3e-73;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MYLTPRYGRSYHDKRSKVDLDNDADAKRYSCPTPNYSVNIREEKLANVVFPRCLL 60
Db 239 myldtpyrgsyhdkrskvdlrldndakryscptpnysvniireelkianvffprcll 298

QY 61 VQRCGNCGGTWNRSCTNSCKTVKKYHEVLQFEPGHIKRRGAKTMAVDIQLDHHE 120
Db 299 vqrcgncgcgtwnrsctnscgtkvkkyhevlqfepghikrrgraktmalvdiqlhdhe 358

QY 121 RDCICSSRP 132
Db 359 rdcicssrppr 370

RESULT 3
AAY96864
ID AAY96864 standard; Protein; 370 AA.
XX
XX AAY96864;
XX
XX 26-SEP-2000 (first entry)
DT
XX
XX SEQ. ID. 37 from WO0034474.
DE
XX
XX Vascular endothelial growth factor; homologue; zveg3; CUB domain;
KW

Query Match 100.0%; Score 737; DB 21; Length 370; Best Local Similarity 100.0%; Pred. No. 1.3e-73; Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MYLDTPTPRGRSVDLRLNDADAKRYSCPTPNYSVNTREELKLANVVFPRCLL 60
 Db 239 myldtptprgrsyhdkrskvdlrldndakryscptpnysvntreelklanvvprrcll 298
 QY 61 VORCGNCGGTNNWRSCTCNSGKTKVKKYHEVLQFEPGHKRRGRKTMALVDIQLDHE 120
 Db 299 vqrcgncgctvnnwrsctcnscktakkyhevlqfepghkrrgraktmalvdlqlhdhe 358
 QY 121 RDCICSSRPPR 132
 Db 359 rdcicssrppr 370

RESULT 5
 AAB60888
 ID AAB60888 standard; protein; 370 AA.
 AC AAB60888;
 XX
 DT 02-APR-2001 (first entry)
 DE -Human VEGF-G protein.
 KW Vascular endothelial growth factor; VEGF; cancer; cell; angiogenesis.
 KW
 XX
 OS Homo sapiens.
 XX
 PN WO200100878-A2.
 XX
 PD 04-JAN-2001.
 XX
 PF 29-JUN-2000; 2000WO-US18085.
 XX
 PR 30-JUN-1999; 99US-0343671.
 XX
 PA (MILL-) MILLENNIUM PHARM INC.
 XX
 PI Gearing DP;
 XX
 DR WPI; 2001-050129/06.
 XX
 PT New vascular endothelial growth factor family member used for diagnosis and treatment of deregulated cell growth e.g. cancer, disorders involving aberrant angiogenesis e.g. psoriasis, and chronic inflammatory diseases -
 XX
 PS Claim 2; Fig 1; 142pp; English.
 XX
 CC The present invention relates to a vascular endothelial growth factor (VEGF) family member, VEGF-G. VEGF-G protein and nucleic acid molecules are used as modulating agents or as targets for developing modulating agents to regulate a variety of cellular processes e.g. cell proliferation, differentiation, migration and wound repair. VEGF-G modulators, i.e. VEGF-G protein, peptide, peptidomimetic or nucleic acid are used to treat a subject with aberrant VEGF-G protein or nucleic acid expression or activity e.g. deregulated cell growth, such as cancer, hyperproliferative bone disorders, disorders involving aberrant angiogenesis e.g. psoriasis, and chronic inflammatory diseases e.g. rheumatoid arthritis. VEGF-G gene expression is inhibited through the administration of antisense molecules or ribozymes and by targeting the regulatory region of VEGF-G to prevent transcription of the gene in target cells.
 XX
 SQ Sequence 370 AA;

Query Match 100.0%; Score 737; DB 22; Length 370;

Best Local Similarity 100.0%; Pred. No. 1.3e-73; Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MYLDTPTPRGRSVDLRLNDADAKRYSCPTPNYSVNTREELKLANVVFPRCLL 60
 Db 239 myldtptprgrsyhdkrskvdlrldndakryscptpnysvntreelklanvvprrcll 298
 QY 61 VORCGNCGGTNNWRSCTCNSGKTKVKKYHEVLQFEPGHKRRGRKTMALVDIQLDHE 120
 Db 299 vqrcgncgctvnnwrsctcnscktakkyhevlqfepghkrrgraktmalvdlqlhdhe 358
 QY 121 RDCICSSRPPR 132
 Db 359 rdcicssrppr 370

RESULT 6
 AAY71128
 ID AAY71128 standard; peptide; 200 AA.
 XX
 AC AAY71128;
 XX
 DT 08-SEP-2000 (first entry)
 DE Human Platelet Derived Growth Factor (PDGF)-D partial polypeptide #1.
 KW Platelet Derived Growth Factor-D; PDGF-D; human; cytostatic; vulnerary; VEGF-G; Vascular Endothelial Growth Factor; antiatherosclerotic; tumour; proliferative; activator; proliferation; differentiation; motility; growth; PDGF-D receptor; antagonist; tissue remodelling; treat; atherosclerosis; wound; metastasis.
 KW
 XX
 OS Homo sapiens.
 XX
 PN WO200027879-A1.
 XX
 PD 18-MAY-2000.
 XX
 PF 10-NOV-1999; 99WO-US26462.
 XX
 PR 10-NOV-1998; 98US-0107852.
 PR 28-DEC-1998; 98US-0113997.
 PR 26-AUG-1999; 99US-0150604.
 PR 04-OCT-1999; 99US-0157108.
 PR 05-OCT-1999; 99US-0157756.
 XX
 XX (LUDW-) LUDWIG INST CANCER RES.
 PA (UYHE-) UNIV HELSINKI LICENSING LTD OY.
 XX
 PI Eriksson U, Aase K, Ponten A, Lee X, Uutela M, Alitalo K;
 PI Oestman A, Heldin C;
 XX
 DR WPI; 2000-376495/32.
 DR N-PSDB; AAD00736.
 XX
 PT Novel polynucleotides encoding a novel growth factor of cells expressing a platelet-derived growth factor, useful for diagnostic and therapeutic applications, e.g. concerning cancer -
 XX
 PS Claim 25; Fig 4; 111pp; English.
 XX
 CC The present sequence is an N-terminally truncated polypeptide of human platelet derived growth factor (PDGF)-D, formally known as Vascular Endothelial Growth Factor (VEGF)-G. It is derived from human foetal lung lamdagt10 cDNA library. It belongs to the VEGF/PDGF family. It functions as an activator of proliferation, differentiation, growth and motility of cells, that express PDGF-D receptor. This sequence is useful for inhibiting the growth of tumours, that express PDGF-D. Expression of PDGF-D and its proteolytic cleavage for generating an activated truncated PDGF-D antagonist is useful for inhibiting tissue remodelling during the invasion of tumour cells into normal cells. PDGF-D may be used to treat wounds, atherosclerosis, metastasis and migration of smooth muscle cells.

XX SQ Sequence 200 AA; Query Match 96.7%; Score 713; DB 21; Length 200; Best Local Similarity 97.7%; Pred. No. 2.9e-71; Mismatches 0; Conservative 0; Indels 0; Gaps 0;

QY 1 MYLDPYRGSRYSYHDKSKVDLRLNDADAKRYSCPTPNYSVNIREEKLANVVFPRCLL 60
 DB 69 MYLDPYRGSRYSYHDKSKVDLRLNDADAKRYSCPTPNYSVNIREEKLANVVFPRCLL 128

QY 61 VQRCGNGCGGTNNRSCNCGTKVYKHYEVLQEPGHIKRRGRKTMALVDIQLDHHE 120
 DB 129 VQRCGNGCGGTNNRSCNCGTKVYKHYEVLQEPGHIKRRGRKTMALVDIQLDHHE 188

QY 121 RDCDICSSRRPPR 132
 DB 189 RDCDICSSRRPPR 200

RESULT 7
 AAB48663
 ID AAB48663 standard; Protein; 370 AA.
 AC AAB48663;
 DT 09-MAR-2001 (first entry)
 DE Mouse growth factor homologue zveg4, SEQ ID NO:53.
 KW Mouse; murine; zveg4; growth factor homologue; VEGF/PDGF family;
 KW CUB domain; PDGF-like activity; mitogenic; osteogenic;
 KW neovascularisation; tissue repair; proliferation; differentiation;
 KW liver damage; neurodegenerative; Alzheimer's disease; multiple sclerosis;
 KW periodontal disease; bone fracture; wound healing; vulnery; ischaemia;
 KW immunomodulation; hepatic.
 OS Mus musculus.
 PN WO2000066736-A1.
 XX 09-NOV-2000.
 PF 03-MAY-2000; 2000WO-US40047.
 PR 03-MAY-1999; 99US-0304216.
 PR 10-NOV-1999; 99US-0164463.
 PR 04-FEB-2000; 2000US-0180169.
 XX (Zymo) ZYMOGENETICS INC.
 PA Gilbert T, Hart CE, Sheppard PO, Gilbertson DG;
 PI WPI; 2000-687541/67.
 DR N-PSDB; AAC81596.
 XX Growth factor homologs and the nucleic acids that encode them, useful
 PT e.g. for treating liver damage, ischemia, multiple sclerosis and
 PT Alzheimer's disease -
 XX Example 19; Page 138-140; 143pp; English.
 PS The invention relates to the human growth factor homologue zveg4
 CC (AAB48653), and nucleic acids encoding it (AAC81595). Zveg4 is a member
 CC of the PDGF (platelet-derived growth factor)/VEGF (vascular endothelial
 CC growth factor) family. Zveg4 has a growth factor domain (AAB48654)
 CC characterised by a PDGF cysteine knot structure, and a CUB domain
 CC (AAB48655) which has a beta barrel structure. Zveg4 has PDGF-like
 CC activity, having mitogenic activity on fibroblasts, vascular smooth
 CC muscle cells and pericytes, and has also been shown to stimulate bone
 CC growth. The invention also relates to fusion proteins comprising human
 CC zveg4 or fragments thereof, particularly human zveg4/human zveg3

CC fusions; expression constructs and host cells comprising human zveg4
 CC nucleic acids; the recombinant expression of human zveg4; an antibody
 CC which binds to human zveg4 or a fragment thereof; a method of activating
 CC a cell-surface PDGF receptor using a zveg4-derived polypeptide; a
 CC method of modulating the proliferation, differentiation, migration or
 CC metabolism of bone cells, comprising exposing bone cells to
 CC zveg4-derived polypeptides; and a method of detecting a genetic
 CC abnormality in the zveg4 gene of a patient. Zveg4 proteins and derived
 CC fragments may be used to stimulate tissue development or repair, or
 CC cellular differentiation or proliferation. They are particularly used for
 CC the treatment or repair of liver damage, and may also be used to
 CC modulate neurite growth (e.g., in the treatment of Alzheimer's disease or
 CC multiple sclerosis). Due to their osteogenic activity, they may be used
 CC in the treatment of periodontal disease and fractures. They may also be
 CC used to enhance expansion and mobilisation of haematopoietic stem cells
 CC and endothelial precursor stem cells, which may be useful in the
 CC treatment of ischaemia, in wound healing, and in the modulation of the
 CC immune system. The present sequence represents mouse zveg4.
 XX SQ Sequence 370 AA;

Query Match 93.1%; Score 686; DB 21; Length 370;
 Best Local Similarity 90.2%; Pred. No. 5.9e-68;
 Mismatches 119; Conservative 7; Mismatches 6; Indels 0; Gaps 0;

QY 1 MYLDPYRGSRYSYHDKSKVDLRLNDADAKRYSCPTPNYSVNIREEKLANVVFPRCLL 60
 DB 239 LYIDTPHYRGSRYSYHDKSKVDLRLNDADAKRYSCPTPNYSVNIREEKLANVVFPRCLL 298

QY 61 VQRCGNGCGGTNNRSCNCGTKVYKHYEVLQEPGHIKRRGRKTMALVDIQLDHHE 120
 DB 299 VQRCGNGCGGTNNRSCNCGTKVYKHYEVLQEPGHIKRRGRKTMALVDIQLDHHE 358

QY 121 RDCDICSSRRPPR 132
 DB 359 RDCDICSSRRPPR 370

RESULT 8
 AAB60895
 ID AAB60895 standard; Protein; 370 AA.
 AC AAB60895;
 DT 02-APR-2001 (first entry)
 XX Human VEGF-G protein.
 DE Vascular endothelial growth factor; VEGF; cancer; cell;
 KW angiogenesis.
 XX Homo sapiens.
 OS WO200100878-A2.
 PN 04-JAN-2001.
 PD 29-JUN-2000; 2000WO-US18085.
 XX 30-JUN-1999; 99US-0343671.
 PR (MILL-) MILLENNIUM PHARM INC.
 PA Gearing DP;
 XX WPI; 2001-050129/06.
 PT New vascular endothelial growth factor family member used for diagnosis
 PT and treatment of deregulated cell growth e.g. cancer, disorders
 PT involving aberrant angiogenesis e.g. psoriasis, and chronic
 PT inflammatory diseases -
 XX

PS Claim 2; Fig 8; 142pp; English.

XX The present invention relates to a vascular endothelial growth factor

CC (VEGF) family member, VEGF-G. VEGF-G protein and nucleic acid

CC molecules are used as modulating agents or as targets for

CC developing modulating agents to regulate a variety of cellular

CC processes e.g. cell proliferation, differentiation, migration and

CC wound repair. VEGF-G modulators, i.e. VEGF-G protein, peptide,

CC peptidomimetic or nucleic acid are used to treat a subject with

CC aberrant VEGF-G protein or nucleic acid expression or activity

CC e.g. deregulated cell growth, such as cancer, hypertrophic bone

CC disorders, disorders involving aberrant angiogenesis e.g. psoriasis,

CC and chronic inflammatory diseases e.g. rheumatoid arthritis. VEGF-G

CC gene expression is inhibited through the administration of antisense

CC molecules or ribozymes and by targeting the regulatory region of VEGF-G

CC to prevent transcription of the gene in target cells.

XX

SQ Sequence 370 AA;

Query Match 92.4%; Score 681; DB 22; Length 370;

Best Local Similarity 89.4%; Pred. No. 2.1e-67;

Matches 118; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

QY 1 MYLDPYRGSRVHDKRSKVDLRLNDADAKRYSCTPRNVSVNIREELKLANVVFPRCLL 60

Db :||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||

239 lyldtphyrgrsyhdkrskvdlrldndvkrystcprnhsvnlreelkltnavffprcll 298

QY 61 VORCGNCGGTVNWRSCNCGTKVKKYHEVLQFEPGHKRGRAKTMALVDIQLDHHE 120

Db ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||

299 vqrcgncgcgtvwnksctcssgktvkkylhevlqfepghkrrgkaknplvdldidhhe 358

QY 121 RDCICSSRRPPR 132

Db ||||||| |||||||

359 rdcicssrrpr 370

RESULT 9

AAAY71132

ID AAY71132 standard; peptide; 66 AA.

XX

AC AAY71132;

XX

DT 08-SEP-2000 (first entry)

XX

DE Human Platelet Derived Growth Factor (PDGF)-D partial polypeptide #3.

XX

KW Platelet Derived Growth Factor-D; PDGF-D; human; cytostatic; vulnerary;

KW VEGF-G; Vascular Endothelial Growth Factor; antiatherosclerotic; tumour;

KW proliferative; activator; proliferation; differentiation; motility;

KW growth; PDGF-D receptor; antagonist; tissue remodelling; treat;

XX atherosclerosis; wound; metastasis.

XX

OS Homo sapiens.

XX

PN WO200027879-A1.

XX

PD 18-MAY-2000.

XX

PF 10-NOV-1999; 99WO-US26462.

XX

PR 10-NOV-1998; 98US-0107852.

PR 28-DEC-1998; 98US-0113997.

PR 26-AUG-1999; 99US-0150604.

PR 04-OCT-1999; 99US-0157108.

PR 05-OCT-1999; 99US-0157756.

XX

PA (LUDW-) LUDWIG INST CANCER RES.

XX (UYHE-) UNIV HELSINKI LICENSING LTD OY.

XX

PI Eriksson U, Aase K, Ponten A, Lee X, Uutela M, Alitalo K;

PI Oestman A, Heldin C;

XX

DR WPI; 2000-376495/32.

XX N-PSDB; AAD00739.

XX

PT Novel polynucleotides encoding a novel growth factor of cells

PT expressing a platelet-derived growth factor, useful for diagnostic and

PT therapeutic applications, e.g. concerning cancer -

PS Disclosure; Fig 2; 111pp; English.

XX

XX The present sequence is the partial C-terminal end polypeptide #3, of

CC human platelet derived growth factor (PDGF)-D, formally known as

CC Vascular Endothelial Growth Factor (VEGF)-G. It is derived from a human

CC expressed sequence tag (EST) A1488780. It belongs to the VEGF/PDGF

CC family. It functions as an activator of proliferation, differentiation,

CC growth and motility of cells, that express PDGF-D receptor. This sequence

CC is useful for inhibiting the growth of tumours, that express PDGF-D.

CC Expression of PDGF-D and its proteolytic cleavage for generating an

CC activated truncated form is useful for regulating receptor binding

CC specificity of PDGF-D. PDGF-D antagonist is useful for inhibiting tissue

CC remodelling during the invasion of tumour cells into normal cells.

CC PDGF-D may be used to treat wounds, atherosclerosis, metastasis and

CC migration of smooth muscle cells.

XX

SQ Sequence 66 AA;

Query Match 51.6%; Score 380; DB 21; Length 66;

Best Local Similarity 100.0%; Pred. No. 6.4e-35;

Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 67 NCGCGTVNWRSCNCGTKVKKYHEVLQFEPGHKRGRAKTMALVDIQLDHHERCDIC 126

Db ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||

1 ncgcgtnvwrscnsgktvkkylhevlqfepghkrrgkraktmalvdldidhhercdic 60

QY 127 SSRPPR 132

Db |||||||

61 ssrppr 66

RESULT 10

AAAB10639

ID AAB10639 standard; Protein; 374 AA.

XX

AC AAB10639;

XX

DT 19-JAN-2001 (first entry)

XX

DE Human VEGF-X protein for expression in mammalian systems.

XX

KW VEGF-X; vascular endothelial growth factor; human; vulnerary; cytostatic;

KW antirheumatic; antiarthritic; antipsoriatic; antidiabetic; treatment;

KW angiogenesis regulator; vascularization regulator; cancer; psoriasis;

KW rheumatoid arthritis; diabetic retinopathy; blood vessel; organ repair;

KW tissue regeneration; tissue repair; wound; dermal ulcer; pressure sore;

XX venous sore; diabetic ulcer; burns; skin graft growth.

XX

OS Homo sapiens.

XX

PN WO200037641-A2.

XX

PD 29-JUN-2000.

XX

PF 21-DEC-1999; 99WO-US30503.

XX

PR 22-DEC-1998; 98GB-0028377.

PR 18-MAR-1999; 99US-0124967.

PR 08-NOV-1999; 99US-0164131.

XX

PA (JANC) JANSSEN PHARM NV.

XX

XX Gordon RD, Sprengel JJ, Yon JR, Dijkmaans JJH, Gosiewska A;

PI Dhanaraj SN, Xu J;

XX


```

FH Key Location/Qualifiers
FT Misc-difference 287 /note= "encoded by AAS"
PN WO200018212-A2.
XX
XX 06-APR-2000.
XX
XX 30-SEP-1999; 99WO-US22668.
XX
XX 30-SEP-1998; 98US-0102461.
XX 12-NOV-1998; 98US-0108109.
XX 03-DEC-1998; 98US-0110749.
XX 18-DEC-1998; 98US-0113002.
XX 21-MAY-1999; 98US-0135426.
XX 15-JUL-1999; 99US-0144022.
XX
XX (LUDW-) LUDWIG INST CANCER RES.
PA (UYHE-) UNIV HELSINKI LICENSING LTD.
XX
XX Eriksson U, Aase K, Lee X, Ponten A, Uutela M, Alitalo K;
PI Oestman A, Heidin C, Betscholz C;
XX
XX WPI; 2000-292954/25.
DR N-PSDB; AAI12524.
XX
XX Novel DNA encoding PDGF-C useful to stimulate or enhance proliferation,
PT differentiation, growth and motility of cells expressing the PDGF-C
PT receptor
XX
XX Disclosure; Fig 4; 135pp; English.
XX
XX The present sequence represents a human platelet-derived growth factor C
CC (PDGF-C) (formally designated VEGF-F) fragment. PDGF-C polypeptides have
CC the ability to stimulate and enhance proliferation or differentiation,
CC and/or growth or motility of cells expressing a PDGF-C receptor.
CC PDGF-C polypeptides can be used in pharmaceuticals for promoting cell
CC proliferation, preferably in combination with one other growth factor
CC and heparin. Pharmaceuticals comprising PDGF-C polypeptides can also
CC be used for stimulating connective tissue or wound healing. The
CC PDGF-C polypeptide can be enzymatically processed to generate the active
CC truncated form of PDGF-C. PDGF-C can also be used to regulate the receptor-binding
CC specificity of PDGF-C. PDGF-C can also be used to promote fibroblast
CC mitogenesis in a mammal and to induce PDGF alpha receptor activation.
CC PDGF-C antagonists can be used to inhibit tumour growth of a tumour
CC expressing PDGF-C in a mammal. Specific types of human tumours, e.g.
CC choriocarcinoma, Wilms tumour, megakaryoblastic leukaemia, lung carcinoma
CC and erythroleukemia, can be identified by testing for expression of
CC PDGF-C. PDGF-C antagonists can also be used to inhibit tissue
CC remodelling during invasion of tumour cells into a normal population of
CC cells. Antagonists can also be used to treat fibrotic conditions,
CC especially found in the lung, kidney or liver.
XX
XX Sequence 318 AA;
SQ
Query Match 44.6%; Score 328.5; DB 21; Length 318;
Best Local Similarity 49.2%; Pred. No. 2.1e-28;
Matches 63; Conservative 20; Mismatches 40; Indels 5; Gaps 3;
QY 1 MYLTPRYGRSY-HDRKSK-VDLDRNLDDAKRYSTPRNYSVINREELKLANVVFPPRC 58
Db 188 llyrptwqlgkafvgrksrvdnlnteervlyscptprnfsvsireelkrtdtfwpgc 247
QY 59 LLVORCGGNGCGCTVNRSTCSNGTKVKKYHEVLQFEPGHIKRRGAKTMAVDIOLDH 118
Db 248 llvkrccgncacclhncnecqvpvskvkkylhevlqrp---ktgvrghksltdvaleh 304
QY 119 HERCDCIC 126
Db 305 heecdcvc 312

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RESULT 13
AAB58438
ID AAB58438 standard; Protein; 339 AA.
XX
XX AAB58438;
XX
XX 14-MAR-2001 (first entry)
XX
XX Lung cancer associated polypeptide sequence SEQ ID 776.
XX
XX Human; lung cancer associated protein; neuroprotective; cytostatic;
XX cardioactive; immunomodulatory; muscular active; vulnerary;
XX gastrointestinal; nephrotropic; antiinfective; gynecological;
XX antibacterial; diagnosis; neural disorder; immune disorder; reproductive;
XX proliferative disorder; wound healing; infectious disease.
XX
XX Homo sapiens.
XX
XX WO200055180-A2.
XX
XX 21-SEP-2000.
XX
XX 08-MAR-2000; 2000WO-US05918.
XX
XX 12-MAR-1999; 99US-0124270.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX (ROSE/) ROSEN C A.
XX
XX Ruben SM;
XX
XX WPI; 2000-587514/55.
XX N-PSDB; AAF18314.
XX
XX Lung cancer associated gene sequences, referred to as lung cancer
XX antigens, useful for treatment, prevention, and diagnosis of disorders
XX such as lung cancer
XX
XX Claim 11; Page 1305-1306; 1425pp; English.
XX
XX Polynucleotide sequences AAF17982 - AAF18424 encode human lung cancer
XX associated proteins represented in AAB58106 - AAB58548. Lung cancer
XX associated proteins and polynucleotide sequences, their agonists, and
XX antagonists may have neuroprotective; cytostatic; cardioactive;
XX immunomodulatory; muscular active general; vulnerary; gastrointestinal
XX general; nephrotropic; antiinfective; gynecological; or antibacterial
XX activity. The invention also includes antibodies specific for the
XX protein or polynucleotide sequences. The lung cancer associated
XX polynucleotide sequences may be used for detection of lung cancer,
XX chromosome identification, as chromosome markers, and for numerous other
XX diagnostic or research purposes. The proteins may be used to treat
XX disorders such as neural, immune, muscular, cardiovascular, renal, and proliferative
XX gastrointestinal, pulmonary, cardiovascular, renal, and proliferative
XX disorders. The proteins may also be used in the treatment of wounds and
XX infectious diseases. Polynucleotide sequences AAF18425 - AAF18433 and
XX peptide AAB58549 are used in the course of the invention for the
XX identification and characterisation of the polynucleotide and protein
XX sequences.
XX
XX Sequence 339 AA;
SQ
Query Match 44.6%; Score 328.5; DB 21; Length 339;
Best Local Similarity 49.2%; Pred. No. 2.2e-28;
Matches 63; Conservative 20; Mismatches 40; Indels 5; Gaps 3;
QY 1 MYLTPRYGRSY-HDRKSK-VDLDRNLDDAKRYSTPRNYSVINREELKLANVVFPPRC 58
Db 209 llyrptwqlgkafvgrksrvdnlnteervlyscptprnfsvsireelkrtdtfwpgc 268
QY 59 LLVORCGGNGCGCTVNRSTCSNGTKVKKYHEVLQFEPGHIKRRGAKTMAVDIOLDH 118
Db 269 llvkrccgncacclhncnecqvpvskvkkylhevlqrp---ktgvrghksltdvaleh 325

```

QY 119 HERCDCIC 126
 Db 326 heeCdvc 333
 RESULT 14
 AAY33679
 ID AAY33679 standard; Protein; 345 AA.
 XX
 AC AAY33679;
 XX
 DT 11-JAN-2000 (first entry)
 XX
 DE Human VEGF-E protein.
 XX
 KW VEGF-E; human; vascular endothelial cell growth factor; wound repair;
 KW treatment; cardiovascular disorder; endothelial disorder; therapy;
 KW tissue generation; regeneration; cardiac hypertrophy; cancer; detection;
 KW angiogenic disorder; age-related macular degeneration; vascular disease;
 KW neovascularization; tumor; gene mapping.
 XX
 OS Homo sapiens.
 XX
 FN WO9947677-A2.
 XX
 PD 23-SEP-1999.
 XX
 PF 10-MAR-1999; 99WO-US05190.
 XX
 PR 17-MAR-1998; 98US-0040220.
 PR 02-NOV-1998; 98US-0184216.
 XX
 PA (GETH) GENENTECH INC.
 XX
 FI Ferrara N, Kuo SS;
 XX
 DR WPI; 1999-580306/49.
 DR N-PSDB; AAZ23691.
 XX
 PT New growth factor polypeptide useful for treating cardiovascular or
 PT endothelial disorders, e.g. cardiac hypertrophy -
 PS Claim 1; Fig 2; 122pp; English.
 CC This invention describes the isolation of a novel human vascular
 CC endothelial cell growth factor-E (VEGF-E) polypeptide which has
 CC tranquilizer, vulnery and cardiant activity. VEGF-E can be administered
 CC therapeutically, especially by expressing encoding polynucleotides, to
 CC treat cardiovascular or endothelial disorders in mammals, especially
 CC humans. It is useful in wound repair and tissue generation and
 CC regeneration, and may especially be used to treat cardiac hypertrophy
 CC It can be combined with a carrier in pharmaceutical compositions, which
 CC can be administered to treat disorders as above. VEGF-E can be used to
 CC screen for antagonists and agonists, and the antagonists administered to
 CC treat angiogenic disorders in mammals (especially humans) e.g. cancer or
 CC age-related macular degeneration. It can be used to generate antibodies,
 CC useful therapeutically as antagonists, as above. The antibodies are also
 CC useful to detect VEGF-E polypeptide, especially to diagnose
 CC cardiovascular, endothelial or angiogenic disorders in mammals (e.g.
 CC vascular disease, or neovascularization associated with tumor formation),
 CC by contacting the antibody with a tissue sample and detecting formation
 CC of an antibody-VEGF-E polypeptide complex. Polynucleotides encoding
 CC VEGF-E can be used to diagnose cardiovascular and endothelial disorders
 CC in mammals, by detecting abnormally high or low VEGF-E gene expression in
 CC tissue samples. They can also be used to diagnose a disease or
 CC susceptibility to a disease related to a mutated form of VEGF-E (e.g. a
 CC cardiovascular, endothelial or angiogenic disorder such as a tumor), by
 CC detecting a mutation in the VEGF-E-encoding sequence isolated from a
 CC sample. They may also be used to produce probes useful to detect related
 CC sequences or for gene mapping. This sequence represents the human VEGF-E
 CC protein described in the method of the invention.

SQ Sequence 345 AA;
 Query Match 44.68; Score 328.5; DB 20; Length 345;
 Best Local Similarity 49.28; Pred. No. 2.3e-28;
 Matches 63; Conservative 20; Mismatches 40; Indels 5; Gaps 3;
 QY 1 MYLDTPRYGRSY-IDRKSK-VLDLRLNDDAKRYSCPTPNYSVNIREELKLANVVFPRC 58
 Db 215. lyrtwqlgkafvgrksrvvdlnllceevrlysectprnfsvsireelkrttdtfwpgc 274
 QY 59 LLVORCGGCGCGTWNRSCTNSGKTVKYHEVLQFEPGHKKRGRKAKTMALVDIQLDH 118
 Db 275 llvkrcgncaccihncnecqcvpskkyhevlqlrp---ktgvrghksltdvaleh 331
 QY 119 HERCDCIC 126
 Db 332 heeCdvc 339
 RESULT 15
 AAY41766
 ID AAY41766 standard; Protein; 345 AA.
 XX
 AC AAY41766;
 XX
 DT 07-DEC-1999 (first entry)
 XX
 DE Human PRO200 protein sequence.
 XX
 KW Human; PRO; EST; expressed sequence tag; PCR primer; hybridisation;
 KW probe; blood coagulation disorder; cancer; cellular adhesion disorder;
 KW secreted protein; transmembrane protein.
 XX
 OS Homo sapiens.
 XX
 FN WO9946281-A2.
 XX
 PD 16-SEP-1999.
 XX
 PF 08-MAR-1999; 99WO-US05028.
 XX
 PR 10-MAR-1998; 98US-0077450.
 PR 11-MAR-1998; 98US-0077632.
 PR 11-MAR-1998; 98US-0077641.
 PR 11-MAR-1998; 98US-0077649.
 PR 12-MAR-1998; 98US-0077791.
 PR 13-MAR-1998; 98US-0078004.
 PR 17-MAR-1998; 98US-0040220.
 PR 20-MAR-1998; 98US-0078886.
 PR 20-MAR-1998; 98US-0078910.
 PR 20-MAR-1998; 98US-0078936.
 PR 20-MAR-1998; 98US-0078939.
 PR 25-MAR-1998; 98US-0079294.
 PR 26-MAR-1998; 98US-0079656.
 PR 27-MAR-1998; 98US-0079663.
 PR 27-MAR-1998; 98US-0079664.
 PR 27-MAR-1998; 98US-0079689.
 PR 27-MAR-1998; 98US-0079728.
 PR 27-MAR-1998; 98US-0079786.
 PR 30-MAR-1998; 98US-0079920.
 PR 30-MAR-1998; 98US-0079923.
 PR 31-MAR-1998; 98US-0080105.
 PR 31-MAR-1998; 98US-0080107.
 PR 31-MAR-1998; 98US-0080165.
 PR 31-MAR-1998; 98US-0080194.
 PR 01-APR-1998; 98US-0080327.
 PR 01-APR-1998; 98US-0080328.
 PR 01-APR-1998; 98US-0080333.
 PR 01-APR-1998; 98US-0080334.
 PR 08-APR-1998; 98US-0081049.
 PR 08-APR-1998; 98US-0081070.
 PR 08-APR-1998; 98US-0081071.

PR 09-APR-1998; 98US-0081195.
PR 09-APR-1998; 98US-0081203.
PR 09-APR-1998; 98US-0081229.
PR 15-APR-1998; 98US-0081817.
PR 15-APR-1998; 98US-0081838.
PR 15-APR-1998; 98US-0081952.
PR 15-APR-1998; 98US-0081955.
PR 21-APR-1998; 98US-0082568.
PR 21-APR-1998; 98US-0082569.
PR 22-APR-1998; 98US-0082700.
PR 22-APR-1998; 98US-0082704.
PR 22-APR-1998; 98US-0082804.
PR 23-APR-1998; 98US-0082767.
PR 23-APR-1998; 98US-0082796.
PR 27-APR-1998; 98US-0083336.
PR 28-APR-1998; 98US-0083322.
PR 29-APR-1998; 98US-0083392.
PR 29-APR-1998; 98US-0083495.
PR 29-APR-1998; 98US-0083496.
PR 29-APR-1998; 98US-0083499.
PR 29-APR-1998; 98US-0083500.
PR 29-APR-1998; 98US-0083545.
PR 29-APR-1998; 98US-0083554.
PR 29-APR-1998; 98US-0083558.
PR 29-APR-1998; 98US-0083559.
PR 30-APR-1998; 98US-0083742.
PR 05-MAY-1998; 98US-0084366.
PR 06-MAY-1998; 98US-0084414.
PR 06-MAY-1998; 98US-0084441.
PR 07-MAY-1998; 98US-0084598.
PR 07-MAY-1998; 98US-0084600.
PR 07-MAY-1998; 98US-0084627.
PR 07-MAY-1998; 98US-0084637.
PR 07-MAY-1998; 98US-0084639.
PR 07-MAY-1998; 98US-0084640.
PR 07-MAY-1998; 98US-0084643.
PR 13-MAY-1998; 98US-0085323.
PR 13-MAY-1998; 98US-0085338.
PR 13-MAY-1998; 98US-0085339.
PR 15-MAY-1998; 98US-0085573.
PR 15-MAY-1998; 98US-0085579.
PR 15-MAY-1998; 98US-0085580.
PR 15-MAY-1998; 98US-0085582.
PR 15-MAY-1998; 98US-0085689.
PR 15-MAY-1998; 98US-0085697.
PR 15-MAY-1998; 98US-0085700.
PR 18-MAY-1998; 98US-0085704.
PR 22-MAY-1998; 98US-0086023.
PR 22-MAY-1998; 98US-0086392.
PR 22-MAY-1998; 98US-0086414.
PR 22-MAY-1998; 98US-0086430.
PR 22-MAY-1998; 98US-0086486.
PR 28-MAY-1998; 98US-0087098.
PR 28-MAY-1998; 98US-0087106.
PR 28-MAY-1998; 98US-0087208.
PR 30-JUL-1998; 98US-0094651.
PR 11-SEP-1998; 98US-0100038.
XX
XX (GETH) GENENTECH INC.
XX
XX
XX Wood WI, Goddard A, Gurney A, Yuan J, Baker KP, Chen J;
XX
XX WPI; 1999-551358/46.
XX N-PSDB; AA234296.
XX
XX New secreted and transmembrane polypeptides and their polynucleotides,
XX useful for treating blood coagulation disorders, cancers and cellular
XX adhesion disorders -
XX
XX Claim 12; Fig 207; 530pp; English.
XX
XX PS
XX PT
XX The present invention describes secreted and transmembrane polypeptides
XX and their polynucleotides. The nucleotide sequences are useful as

CC sources of probes, primers, for chromosome mapping, and for generation
CC of antisense sequences. They can also be used to create transgenic
CC animals. The proteins can be used to treat a variety of diseases and
CC disorders, depending on their function. Diseases that may be treated
CC include blood coagulation disorders, cancers and cellular adhesion
CC disorders. They may also be used to raise antibodies. AA23891 to
CC AA234338, and AA41685 to AA41774 represent polynucleotide and
CC polypeptide sequence given in the exemplification of the present
CC invention.
XX
XX Sequence 345 AA;
SQ
Query Match 44.6%; Score 328.5; DB 20; Length 345;
Best Local Similarity 49.2%; Pred. No. 2.3e-28;
Matches 63; Conservative 20; Mismatches 40; Indels 5; Gaps 3;
QY 1 MYLDTPRYGRSY-HDRKSK-VDLRLNDKAKRYSCPTPRNYSVNIREEELKLANVVFPRC 58
DB 215 lyrtwtgllgkafvgrksrvdnliltteevrlyscptprnfsvireelkrtditwpgc 274
QY 59 LLVQRCGGNGCGCTVNRSTCNSGKTVKKYHEVLOFEPGHKRRGKRAKTMALVDIOLDH 118
DB 275 llvrcggnccclhncqcqvpvsktkkyhevlqlrp---ktgvrghksitdvalch 331
QY 119 HERDCIC 126
DB 332 heecdcvc 339

Search completed: September 26, 2001, 15:15:39
Job time: 30 sec

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 Date: Sep 26, 2001 8:31 PM
 About: Results were produced by the GenCore software, version 4.5,
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Command line parameters:

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 -MINMATCH=0.100 -LOOPCL=0.000 -LOOPEXT=0.000 -GAPOP=4.500
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 -FGAEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500 -DELOP=6.000
 -DELEXT=7.000 -START=1 -MATRIX=blosum62 -TRANS=human40.cdi
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 -ALIGN=15 -MODE=LOCAL -OUTPMT=pfs -NORM=ext -MINLEN=0
 -MAXLEN=200000000 -USER=US09662783 -CGN1_1_2918 -NCPU=6
 -ICPU=3 -LONGLOG -NO_XLPXY -WAIT -THREADS=1

Search information block:

Query: us-09-662-783-4

Query length: 132

Database: EST:

Database sequences: 10228115

Database length: 431459454

Search time (sec): 1311.130000

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gb_est53:AA968905	+	460.00	940.41	2.9e-43	560	AW968905 EST30981 MAGE resequ
gb_est8:AA488780	+	380.00	778.74	2.9e-34	360	AA488780 aa54c10.r1 NCI_CGAP
gb_est8:BF021679	+	324.50	659.84	1.2e-27	523	BF021679 uy50f05.y1 NCI_CGAP
gb_est102:BG609411	+	322.50	655.08	2.3e-27	556	BG609411 33251 MARC IPTG Sus
gb_est84:BF151355	+	309.50	627.96	7.4e-26	564	BF151355 uz15b12.y1 NCI_CGAP
gb_est28:AL047637	+	301.50	617.48	2.8e-25	304	AL047637 DKFZP586J0421.r1 586
gb_est81:BE958470	+	294.50	597.57	3.6e-24	523	BE958470 601644787F1 NIH_MGC
gb_gss4:CN60488A	-	291.00	583.53	2.2e-23	1036	AL304867 Tetradon nigriviridis
gb_est98:BG243001	+	275.50	552.65	1.2e-21	910	BG243001 602355974F1 NCI_CGAP
gb_est83:BF102859	+	272.50	551.24	1.4e-21	851	BF102859 601646827F1 NIH_MGC
gb_est82:BF031624	+	272.50	545.99	2.7e-21	950	BF031624 601558104F1 NIH_MGC
gb_est82:BF011835	+	264.00	535.82	1.0e-20	447	BF011835 us37d10.y1 Soares.MN
gb_gss3:CN5024MX	-	231.00	460.65	1.5e-16	877	AL180978 Tetradon nigriviridis
gb_gss23:AZ237000	-	201.00	405.85	1.7e-13	413	AZ237000 RCI-23-7102.TV RCI-2
gb_est91:BF670092	+	194.00	383.89	2.9e-12	874	BF670092 602119417F1 NIH_MGC
gb_est80:BE914552	+	184.00	364.02	3.7e-11	799	BE914552 60165653F1 NCI_CGAP
gb_est84:BF163629	+	179.00	352.44	1.6e-10	902	BF163629 601769732F1 NCI_CGAP
gb_est17:BG118707	+	178.50	350.70	2.0e-10	968	BG118707 602348280F1 NIH_MGC
gb_est15:AT020581	+	163.00	329.38	3.2e-09	324	AT020581 us96c08.r1 Soares.MN
gb_est73:BE374398	+	135.00	266.55	1.0e-05	521	BE374398 601227568F1 NCI_CGAP
gb_est44:AW210331	+	124.00	243.91	0.0002	511	AW210331 ul53f09.y1 Rashbass m
gb_gss4:CN5030JLN	-	124.00	239.13	0.0003	828	AL261284 Tetradon nigriviridis
gb_gst4:AW977062	-	120.50	235.36	0.0005	582	AW977062 EST389171 MAGE resequ
gb_est14:AA759138	-	108.50	213.57	0.0089	425	AA759138 ah78f03.s1 Soares.Les
gb_est83:BF117246	+	105.50	219.39	0.0042	126	BF117246 uz07a06.y1 NCI_CGAP
gb_gss31:AE686072	+	95.00	178.59	0.7902	858	AZ686072 ENTK57TF Entamoeba h
gb_est99:BG35361	+	92.00	178.56	0.7929	459	BG35361 947043E01.y2 947 - 2
gb_est17:AI174183	+	91.00	178.12	0.8385	389	AI174183 uc07b07.r1 Soares.MN
gb_est30:AA085049	+	91.00	175.56	1.17	504	AA085049 AU085049 Cryptomeria
gb_est7:AA425486	+	91.00	175.46	1.18	509	AA425486 zv46b06.r1 Soares.tot
gb_est103:DA9188	+	90.50	177.16	0.9485	386	DA9188 RICS16279A Rice green sh
gb_est87:BF423344	+	90.00	174.11	1.40	473	BF423344 sr37b04.y1 Gm-cl051 G
gb_est83:BF073247	+	90.00	172.91	1.64	534	BF073247 219851 MARC 2BOV Bos
gb_est22:AI583995	+	90.00	169.35	2.58	765	AI583995 ts08c03.x1 NCI_CGAP
gb_est22:BF262012	+	90.00	168.62	2.84	823	BF262012 HV_CEA002N05f Hordeu
gb_est74:BE424082	-	89.50	173.16	1.59	469	BE424082 WHE0068.G05_M102S Whea
gb_est53:AW314212	+	89.00	173.26	1.56	418	AW314212 EST345516 Normalized
gb_est4:AA240232	+	89.00	173.00	1.62	429	AA240232 my24b02.r1 Barstead m
gb_est7:AA420061	+	89.00	171.91	1.86	479	AA420061 vf50b05.r1 Soares.MN
gb_est89:BF523368	+	89.00	171.48	1.96	500	BF523368 UI-R-G0-uh-c-05-0-UI.R

gb_est80:BE864788	+	89.00	170.56	2.21	549	BE864788 UI-M-BH1-alu-c-12-0
gb_est48:AW555889	-	89.00	170.19	2.32	570	AW555889 L0260G12-3 Mouse Ne
gb_est87:BF448004	-	89.00	170.19	2.32	570	BF448004 nae3a0a08.x1 Lupski
gb_est96:BG087899	+	89.00	169.84	2.42	590	BG087899 H3146C02-5 NIA Mous

seq_name: gb_hlc:AK003359

seq_documentation_block:

LOCUS AK003359 1796 bp mRNA HTC 08-FEB-2001
 DEFINITION Mus musculus 18 days embryo cDNA, RIKEN full-length enriched
 library, clone:1110003109, full insert sequence.

ACCESSION AK003359

VERSION AK003359.1 GI:12833975

KEYWORDS CAP trapper.

SOURCE Mus musculus (strain:C57BL/6J) 18 days embryo cDNA to mRNA,

clone.lib:RIKEN full-length enriched mouse cDNA library

clone:1110003109.

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (sites)

AUTHORS Carninci,P. and Hayashizaki,Y.

TITLE High-efficiency full-length cDNA cloning

JOURNAL Methods Enzymol. 303, 19-44 (1999)

REFERENCE 2 (sites)

AUTHORS Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,

Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.

TITLE Normalization and subtraction of cap-trapper-selected cDNAs to

prepare full-length cDNA libraries for rapid discovery of new genes

Genome Res. 10 (10), 1617-1630 (2000)

20499374

REFERENCE 3 (sites)

AUTHORS Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,

Konno,H., Akiyama,J., Nishi,K., Kitsuai,T., Tashiro,H., Itoh,M.,

Kikuchi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T.,

Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T.,

Kashiwagi,K., Fujiwaka,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,

Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T.,

Matsura,S., Okazaki,Y., Muramatsu,M., Inoue,Y. and Hayashizaki,Y.

TITLE RIKEN integrated sequence analysis (RISA) system--384-format

sequencing pipeline with 384 multicapillary sequencer

Genome Res. 10 (11), 1757-1771 (2000)

20530913

REFERENCE 4 (sites)

AUTHORS The RIKEN Genome Exploration Research Group Phase II Team and

FANTOM Consortium.

TITLE Functional annotation of a full-length mouse cDNA collection

Nature 409, 685-690 (2001)

REFERENCE 5 (bases 1 to 1796)

AUTHORS Adachi,J., Aizawa,K., Akahira,S., Akimura,T., Aono,H., Arai,A.,

Arakawa,T., Carninci,P., Fukuda,S., Fukunishi,Y., Furuno,M.,

Imotani,K., Ishii,Y., Itoh,M., Kato,H., Kawai,J., Hori,F.,

Kojima,Y., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T.,

Miyazaki,A., Nishi,K., Nomura,K., Numasaki,R., Ohno,M., Okazaki,Y.,

Okido,T., Owa,C., Saito,H., Saito,R., Sakai,C., Sano,H., Sano,H.,

Sasaki,D., Shibata,K., Shibata,Y., Shinagawa,A., Shiraki,T.,

Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F.,

Tanaka,T., Tejima,Y., Toya,T., Yamamura,T., Yasunishi,A.,

Yoshida,K., Yoshino,M., Muramatsu,M. and Hayashizaki,Y.

TITLE Direct Submission

Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of

Physical and Chemical Research (RIKEN), Laboratory for Genome

Exploration Research Group, RIKEN Genomic Sciences Center (GSC),

RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,

Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp,

URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,

Fax:81-45-503-9216)

COMMENT Please visit our web site (<http://genome.gsc.riken.go.jp/>) for

further details.

cDNA library was prepared and sequenced in Mouse Genome

Encyclopedia Project of Genome Exploration Research Group in Riken

Genomic Sciences Center and Genome Science Laboratory in RIKEN.


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seq_documentation_block:
LOCUS AA488780 360 bp mRNA EST 15-AUG-1997
DEFINITION aa54c10.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:824754 5',
mRNA sequence.
ACCESSION AA488780
VERSION AA488780.1 GI:2218382
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 360)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman,
Ph.D., Gerald Marti, M.D.
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Seq primer: -28ml3 rev1 ET from Amersham
High quality sequence stop: 358.
FEATURES
source
1..360
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:824754"
/clone_lib="NCI_CGAP_GCB1"
/tissue_type="germinal center B cell"
/lab_host="DH10B"
/notes="Vector: p7T73D-Pac (Pharmacia) with a modified
polylinker; Site.1: Not I; Site.2: Eco RI; 1st strand cDNA
was prepared from human tonsillar cells enriched for
germinal center B cells by flow sorting (CD20+, IgD-),
provided by Dr. Louis M. Staudt (NCI), Dr. David Allman
(NCI) and Dr. Gerald Marti (CBER). cDNA synthesis was
primed with a Not I - oligo(dT) primer
[5'-TGTTACCAATCTGAAGTGGAGCGCGCTCATTTTTTTTTTTT-3'
1. Double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified p7T73 vector. Library
went through one round of normalization, and was
constructed by Bento Soares and M. Fatima Bonaldo."
BASE COUNT 108 a 77 c 86 g 89 t
ORIGIN
alignment_scores:
Quality: 380.00 Length: 66
Ratio: 5.758 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000
alignment_block:
US-09-662-783-4 x AA488780
Align seg 1/1 to: AA488780 from: 1 to: 360
67 AsnCysGlyCysGlyThrValAsnTrpArgSerCysThrCysAsnSerG1 83
|||||
1 AATGTGGTGTGGAACTGTCAACTGGAGGTCTGCACATGCAATTCAGG 50
|||||
83 YLysThrValLYsLysTyrHisGluValLeuGlnPheGluProGlyHisI 100
|||||
51 GAACACCGTGAAGATATCATGAGGTATTACAGTTTGAGCCCTGGCCACA 100
|||||
100 leLysArgArgGlyArgAlaLysThrMetAlaLeuValAspIleGlnLeu 116
|||||

```

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101 TCAAGAGGAGGGGTAGAGCTAAGACCATGGCTAGTTCACATCCAGTTG 150
|||||
117 AspHisHisGluArgCysAspCysIleCysSerSerArgProProArg 132
|||||
151 GATCACCATGAGGATGTATTGTATCTGCAGCTCAAGACCACTCGA 198
|||||
seq_name: gb_est82:BF021679
seq_documentation_block:
LOCUS BF021679 523 bp mRNA EST 29-DEC-2000
DEFINITION uy50f05.y1 NCI_CGAP_Lu30 Mus musculus cDNA clone IMAGE:3663009 5',
similar to FR:Q9QY71 Q9QY71 FALLOTEIN. ; mRNA sequence.
ACCESSION BF021679
VERSION BF021679.1 GI:10753011
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 523)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
image.llnl.gov/image/html/iresources.shtml
MG1:1423777
Seq primer: -40RP from Gibco
High quality sequence stop: 452.
FEATURES
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1..523
/organism="Mus musculus"
/strain="CZECH II"
/db_xref="taxon:10090"
/clone="IMAGE:3663009"
/clone_lib="NCI_CGAP_Lu30"
/tissue_type="tumor, metastatic to mammary"
/lab_host="DH10B"
/notes="Organ: Lung; Vector: pCMV-SPORT6; Site.1: NotI;
Site.2: SalI; transgenic model WNT-1, expression driven by
MMTV-LTR enhancer; Cloned unidirectionally. Primer: Oligo
dT. Library constructed by Life Technologies.
Investigator providing samples: Gilbert Smith, NIH"
BASE COUNT 143 a 116 c 139 g 125 t
ORIGIN
alignment_scores:
Quality: 324.50 Length: 128
Ratio: 3.311 Gaps: 3
Percent Similarity: 76.562 Percent Identity: 48.438
alignment_block:
US-09-662-783-4 x BF021679
Align seg 1/1 to: BF021679 from: 1 to: 523
1 MetTyrLeuAspThrProArgTyrArgGlyArgSerTyr...HisAspAr 16
|||||
131 CTCTACAGCCACATGGCAGCTTTGGCAGGCTTCCTGTATGGAA 180
|||||
16 GlySerLys...ValAspLeuAspArgLeuAsnAspAlaLysArgT 32
|||||
181 AAAAAGCAAGTGGTGAATCTGAATCTCCTCAAAGGAGGTAACACTCT 230
|||||

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32 yrSerCysThrProArgAsnTyrSerValAsnIleArgGluGluLeuLys 48
|||||
231 ACAGCTGCACACCCCGGAACCTCTCAGTGTCCATCGGGAAGAGCTAAAG 280
|||||
49 LeuAlaAsnValValPhePheProArgCysLeuLeuValGlnArgCysG1 65
|||||
281 AGGACAGATACCATATTCTGCGCCAGGTGTCTCTCTGGTCAAGCGCTGTGG 330
|||||
65 yGlyAsnCysGlyCysGlyThrValAsnTyrArgSerCysThrCysAsnS 82
|||||
331 AGGAAATGTCCCTGTGTCTCCATAATTCGAATGATGTCTCAGTGTGCC 380
|||||
82 erGlyLysThrValLysLysTyrHisGluValLeuGlnPheGluProGly 98
|||||
381 CACGTAAGTTACAAAAGTACCATGAGTCCCTTCAGTTGAGACCA... 427
|||||
99 HistLeysArgArgGlyArgAlaLysThrMetAlaLeuValAspIleG1 115
|||||
428 .....AAAACGTGGAGTCAAGGATTCGATAAGTCACTCACTGATGTGGC 471
|||||
115 nLeuAspHisGluArgCysAspCysIleCys 126
|||||
472 TCTGGAACACACCGAGGAATGACTGTGTGT 505
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seq_name: gb_est102:BG609411

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seq_documentation_block: 556 bp mRNA EST 17-APR-2001
LOCUS BG609411
DEFINITION 323251 MARC 1PIG Sus scrofa cDNA 5', mRNA sequence.
ACCESSION BG609411
VERSION BG609411.1 GI:13659390
KEYWORDS EST.
SOURCE Pig.
ORGANISM Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE 1 (bases 1 to 556)
AUTHORS Fahrtenkrug,S.C., Freking,B.A., Rohrer,G.A., Smith,T.P.L., Casas,E.,
Stone,R.T., Heaton,M.P., Grosse,W.M., Bennett,G.A., Laegreid,W.W.
and Keele,J.W.
TITLE Design and use of two pooled tissue normalized cDNA libraries for
EST discovery in swine
JOURNAL Unpublished (2000)
COMMENT Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -mismatch 12 options.
PCR Primers
FORWARD: AGGAACACAGCTATGACCAT
BACKWARD: GTTTCACGATCAGCAGC
Plate: 98 row: P column: 8
Seq primer: ATTTAGTGCACACTATAG.

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FEATURES

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/tissue_type="pooled"
/lab_host="DH10B"
/note="Vector: pCMV SPORT6; Site_1: XbaI; Site_2: XhoI;
Library made from pooled tissue from day 11, 13, 15, 20,
and 30 embryos."
BASE COUNT 139 a 153 c 141 g 123 t
ORIGIN

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alignment_scores:

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Quality: 322.50 Length: 128
Ratio: 3.291 Gaps: 3
Percent Similarity: 76.562 Percent Identity: 48.438

alignment_block:
US-09-662-783-4 x BG609411 ..
Align seg 1/1 to: BG609411 from: 1 to: 556

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182 CTATACAGGCGCAACTGTGGCAACTCTCGGCAAGGCTTTTGTTCGGAAG 231
|||||
16 gLysSerLys...ValAspLeuAspArgLeuAsnAspAspAlaLysArgT 32
|||||
232 AAATCCAGAGTGTGGATCTGAACCTTCTCAAGAAGAAGTGAAGCTAT 281
|||||
32 yrSerCysThrProArgAsnTyrSerValAsnIleArgGluGluLeuLys 48
|||||
282 ACAGCTGCACCCCTAGGAACCTTTTCAGTGTCTATCAGGGAAGAGCTGAAG 331
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49 LeuAlaAsnValValPhePheProArgCysLeuLeuValGlnArgCysG1 65
|||||
332 AGAACACACACCATCTTCTGCGCAGGCTGCTCTCTGTCGCAAGCGTTGTGG 381
|||||
65 yGlyAsnCysGlyCysGlyThrValAsnTyrArgSerCysThrCysAsnS 82
|||||
382 CGGAACGTGTGCTGCTCCATGTCACACCTGCATGAGTGTCTCAGTGTGCC 431
|||||
82 erGlyLysThrValLysLysTyrHisGluValLeuGlnPheGluProGly 98
|||||
432 CCAGCAAGTCAACCAAGAAATATCAGGAGTCTTCAGTTGAGACCC... 478
|||||
99 HistLeysArgArgGlyArgAlaLysThrMetAlaLeuValAspIleG1 115
|||||
479 .....AAGACAGTGTCCGGGGGCTGCACAAGTCCCTCACCGAGCTGGC 522
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115 nLeuAspHisGluArgCysAspCysIleCys 126
|||||
523 CCTGGAGCACACCGAGGAGTGTGACTGCGTGTGC 556

seq_name: gb_est84:BF151355

seq_documentation_block:
LOCUS BF151355 564 bp mRNA EST 29-DEC-2000
DEFINITION uz15b12.y1 NCI-CGAP_Mam5 Mus musculus cDNA clone IMAGE:3669119 5'
similar to TR:Q9QY71 Q9QY71 FALLOTEIN.; mRNA sequence.
ACCESSION BF151355
VERSION BF151355.1 GI:11032750
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
REFERENCE 1 (bases 1 to 564)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cygapb@mail.nih.gov
CDNA Library preparation: Lohar Hennighausen Ph.D., Robin Humphreys
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
image.lnl.gov/image/html/iresources.shtml
MGI:1429887
Seq primer: -40RP from Gibco
High quality sequence stop: 436.
Location/Qualifiers

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FEATURES

Align seg 1/1 to reverse of: CNS04S8A from: 1 to: 1036


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20 ValaspLeuAspArgLeuAsnAspAlaLysArgTyrSerCysThrPr 36
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406 GTGATGCTCAACCGCTCCATGATGTTCAAGCGCTACAGCTGACCC 357

36 oArgAsnTyrSerValAsnIleArgGluGluLeuLysLeuAlaAsnValV 53
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
356 CGGTAACTACTGTAAATCTCAAAAGAGCTAAGGCCACAAACGCTA 307

53 alPhePheProArgCysLeuLeuValGlnArgCysGlyGlyAsnCysGly 69
:::|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
306 TTTTCTCCACGCTGTTGCTTTGACACGATGTTGGTGGCAACTGTGA 257

70 CysGlyThrValAsnTyrArgSer..CysThrCysAsnSerGlyLysThr 85
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
256 TGTGGACCAACGCACTGGAATAACACTGCGCTGTCAGGCCGCCAAATCA 207

86 ValLysLysTyrHisGluVal 92
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206 GCACCAAACTACATGAAGTA 186

seq_name: gb_est98:BG243001

seq_documentation_block: 910 bp mRNA EST 13-FEB-2001
LOCUS BG243001
DEFINITION 60235974F1 NCI_CGAP_Mam1 Mus musculus cDNA clone IMAGE:4483938 5',
mRNA sequence.
ACCESSION BG243001
VERSION BG243001.1 GI:12752725
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 910)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10323 row: d column: 19
High quality sequence stop: 690.
FEATURES
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1..910
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/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:4483938"
/clone_lib="NCI_CGAP_Mam1"
/tissue_type="tumor, biopsy sample"
/dev_stage="3 months, virgin"
/lab_host="DH10B"
/notes="Organ: mammary; Vector: pCMV-SPORT6; Site_1: Sall;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"
BASE COUNT 242 a 220 c 250 g 198 t
ORIGIN

alignment_scores:
Quality: 275.50 Length: 119
Ratio: 2.900 Gaps: 3
Percent Similarity: 79.832 Percent Identity: 51.261

alignment_block:
US-09-662-783-4 x BG243001

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Align seg 1/1 to: BG243001 from: 1 to: 910

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10 GlyArgSerTyr...HisAspArgLysSerLys...ValaspLeuAspAr 24
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149 GCGAAGGCTTTCTGTATGGGAAAGAAAGCAAGTGGTGAATCTGAATCT 198

24 gLeuAsnAspAspAlaLysArgTyrSerCysThrProArgAsnTyrSerV 41
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
199 CCTCAAGGAAGAGGTAAACTCTACAGCTGCACACCCCGGAACCTCTCAG 248

41 alAsnIleArgGluGluLeuLysLeuAlaAsnValValPhePheProArg 57
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
249 TGTCCATACGGGAAGAGCTAAAGAGACAGATACCATATTTCTGGCAGGT 298

58 CysLeuLeuValGlnArgCysGlyGlyAsnCysGlyCysGlyThrValAs 74
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
299 TGTCTCCTGGTCAAGCGCTGTGGAGAAA..TGTGCTGTGTCTCCATAA 347

74 nTrrArgSerCysThrCysAsnSerGlyLysThrValLysLysTyrHisG 91
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
348 TTGCAATGAATGTCAGTGTGCCACGTAAGTTACAAAAAAGTACCATG 397

91 luValLeuGlnPheGluProGlyHisIleLysArgArgGlyArgAlaLys 107
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
398 AGGTCTCTTCAGTTGAGACCA.....AAAACCTGAGTCAAGGGA.TTG 437

108 ThrMetAlaLeuValAspIleGlnLeuAspHisGluArgCysAspCy 124
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
438 CATAAGTCACTCACTGATGTGGCTCTGGAAACACACGAGGAATGTGAC 487

124 sileCys 126
488 TGTGTGT 494

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seq_name: gb_est93:BF102859

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seq_documentation_block:
LOCUS BF102859 851 bp mRNA EST 19-OCT-2000
DEFINITION 601646827F1 NIH_MGC_60 Homo sapiens cDNA clone IMAGE:4073095 5',
mRNA sequence.
ACCESSION BF102859
VERSION BF102859.1 GI:10885385
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 851)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
CDNA Library Preparation: CLONETECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM921 row: f column: 08
High quality sequence stop: 529.
FEATURES
source
1..851
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4073095"
/clone_lib="NIH_MGC_60"
/tissue_type="adenocarcinoma"
/lab_host="DH10B (T1 phage-resistant)"
/notes="Organ: prostate; Vector: pDNR-LIB (Clontech);
Site_1: SfiI (ggccctatggcc); Site_2: SfiI (ggccattatggcc)

```



```

KEYWORDS
SOURCE      house mouse.
ORGANISM     Mus musculus
REFERENCE    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
TITLE        1 (bases 1 to 447)
            NCI-CCGAP http://www.ncbi.nlm.nih.gov/ncicgap.
            National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
JOURNAL      Unpublished (1997)
COMMENT      Contact: Robert Strausberg, Ph.D.
            Email: ccgaps-r@mail.nih.gov
            cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo
            , Ph.D.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Washington University Genome Sequencing Center
            Clone distribution: NCI-CCGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            image.llnl.gov/image/html/iresources.shtml

MGI:1064727
Seq primer: -40RP from Gibco
High quality sequence stop: 402.
            Location/Qualifiers
            1..447
            /organism="Mus musculus"
            /db_xref="taxon:10090"
            /clone="IMAGE:3169267"
            /clone_lib="Soares_NBEBA_branchial_arch"
            /tissue_type="branchial arches"
            /dev_stage="embryo, 10.5 dpc"
            /lab_host="DH10B (phage resistant)"
            /note="vector: pT7T3p-Pac (Pharmacia) with a modified
            polylinker; Site_1: NotI; Site_2: EcoRI; 1st strand cDNA
            was primed with a Not I - oligo(dT) primer [5'
            TGTTCACCACTGAAGTGGGCGCCGATGTCATTTTCTTTTCTTTTCTTTT
            3']; double-stranded cDNA was ligated to Eco RI adaptors
            (Pharmacia), digested with Not I and cloned into the Not
            I and Eco RI sites of the modified pT7T3 vector. Library
            constructed and normalized by Bento Soares and M.Patima
            Bonaldo."
BASE COUNT   126 a 104 c 108 g 109 t
ORIGIN
            alignment_scores:
            Quality: 264.00 Length: 99
            Ratio: 3.342 Gaps: 2
            Percent Similarity: 79.798 Percent Identity: 51.515
alignment_block:
US-09-662-783-4 x BF011835
Align seg 1/1 to: BF011835 from: 1 to: 447
1 MetTyrLeuAspThrProArgTyrArgGlyArgSerTyr...HisAspAr 16
:::||||| ||| :::: |||:::||||: |||:::||||: |||:::
115 CTCACAGCCACATCGGACGCTTTTGGCAAGGCTTCTCTGTATGGGA 164
16 glySerLys...ValAspLeuAspArgLeuAsnAspAspAlaLysArg 32
:::||||| |||:::||||: |||:::||||: |||:::||||: |||:::
165 AAAACGAAGTGGTGAATCTGAATCTCCTCAAGGAAGAGGTAACACTCT 214
32 yfSerCysThrProArgAsnTyrSerValAsnIleArgGluGluLeuLys 48
|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
215 ACAGCTGCACACCCGCGACTTCTCAGTGTCCTCAGGGAAGAGCTAAAG 264
49 LeuAlaAsnValValPhePheProArgCysLeuLeuValGlnArgCysG 65
:::||||| |||:::||||: |||:::||||: |||:::||||: |||:::
265 AGGACAGATACCATATCTTGGCCAGGTGTCTCTGTGTCAGGCGCTGTGG 314
65 yGlyAsnCysGlyCysGlyThrValAsnTrpArgSerCysThrCysAsn 82
|||||:::||||: ||| :::: |||:::||||: |||:::||||: |||:::

```

```

315 AGGAATTTGTGCTGTGTCTCCATAAATGCAATGAATGTCAGTGTGTCC 364
82 erGlyLysThrValLysTyrHisGluValLeuGlnPheGluPro 97
365 CACGTAAAGTTACAAAAAGTACCATGAGGTCTCTTCAGTTGAGACCA 411
seq_name: gb_gss3:CNS024MX
seq_documentation_block:
LOCUS      CNS024MX      877 bp      DNA      GSS      12-MAY-2000
DEFINITION Tetraodon nigroviridis genome survey sequence PUC-Ori end of clone
235A22 of library G from Tetraodon nigroviridis, genomic survey
sequence.
ACCESSION  AL180978
VERSION     AL180978.1 GI:7819035
KEYWORDS    GSS; genome survey sequence.
SOURCE      Tetraodon nigroviridis.
ORGANISM    Tetraodon nigroviridis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
            Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
            Tetraodontidae; Tetraodon.
REFERENCE   1 (bases 1 to 877)
AUTHORS     Roest-Crolius,H., Jaillon,O., Dasilva,C., Fizames,C., Fisher,C.,
            Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and
            Weissenbach,J.
TITLE       Characterization and repeat analysis of the compact genome of the
            freshwater pufferfish Tetraodon nigroviridis
JOURNAL     Unpublished
REFERENCE   2 (bases 1 to 877)
AUTHORS     Roest-Crolius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,
            Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F.,
            Saurin,W. and Weissenbach,J.
TITLE       Human gene number estimate provided by genome wide analysis using
            Tetraodon nigroviridis DNA sequence
JOURNAL     Unpublished
REFERENCE   3 (bases 1 to 877)
AUTHORS     Genoscope.
TITLE       Direct Submission
JOURNAL     Submitted (12-APR-2000) to the EMBL/GenBank/DBJ databases
COMMENT     This sequence is a single read and was generated as part of a large
            scale clone-end sequencing project of the Tetraodon nigroviridis
            genome. For more information, please take a look at
            http://www.genoscope.cns.fr/tetraodon.
FEATURES
            source
            1..877
            /organism="Tetraodon nigroviridis"
            /db_xref="taxon:99883"
            /clone="235A22"
            /clone_lib="G"
            /note="Genoscope sequence ID : COAG235BALLSP1-end :
            PUC-Ori"
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            Quality: 231.00 Length: 211
            Ratio: 2.625 Gaps: 5
            Percent Similarity: 41.706 Percent Identity: 26.540
alignment_block:
US-09-662-783-4 x CNS024MX/rev
Align seg 1/1 to reverse of: CNS024MX from: 1 to: 877
25 LeuAsnAspAlaLysArgTyrSerCysThrProArgAsnTyrSerVa 41
|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
651 CTGAGGATGAAGTGGACTGTACACTGCACACCGCGCAACTTCTGT 602
41 lAsnIleArgGluGluLeuLysLeuAlaAsnValValPhePheProArgC 58
|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
601 GTCTTTGCGTGAGAGCTGAAGAGGACCGATGTAATTTTCTGCCAAGCT 552

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58 ysLeuLeuValGlnArgCysGlyAsnCysGlyCysGlyThrValAsn 74
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551 GCCTCCTGGTGAATCGCTGTGGCGAAACTGCGCTGCTCTCACGCC 502
75 TrpArgSerCysThrCysAsnSerGlyLysThrValLysLysTyrHisG1 91
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
501 TGCATGACTGCCATCGCTTCCACCAGGCTCACGAAGAATATCATGA 452
91 uVal.....LeuGlnPheGluProGlyH 99
|||||:|||||:|||||:|||||:|||||:|||||:
451 GGTAAATGCTAGCACTTCACCTGAGGATGATGTTTCCGTTTGCTGCC 402
99 isleLys.....ArgArgLys..... 104
|||||:|||||:|||||:|||||:|||||:|||||:
401 TTTTAAAGATTTTGAATGCGCGTTTGGAACTTCACAAATTTCTGCT 352
104 ..... 104
351 GCCATTACACAATACTACATKCCAGACACTGTGAAATGTACAAATACTT 302
105 ..... 108
301 ATCTGACTTGAATAATTCAGATCTGAGACGAAATCCACTTACACTGCAA 252
108 ..... 108
251 TATTTGTTTAAACAAACAAATCAACAAATCAAGACCAAGCTAAATG 202
108 ..... 108
201 GCATTTGATGATAATATGATCAGCTTTAAGATGAAATGTTTGATGCCA 152
108 ..... 108
151 ACATGTTGTGCAGGTTCTGCTGTAACATCGAATGGTGGCAAGGCC 102
109 .....MetAlaLeuValAspLleGlnLeuAspHisHisGluArgCysAsp 123
|||||:|||||:|||||:|||||:|||||:|||||:
101 TGCAGAATCGTTGACGAGCTGCCCTTAGAACACACCAGCAAGAAATGCGCC 52
124 CysLecCysSerSerArg.....ProPro 131
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51 TGCCTGTGTAAGATGACTGGGACTGACCTCCG 19

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seq_name: gb_gss23:AZ237000

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seq_documentation_block: 413 bp DNA GSS 14-JUN-2000
LOCUS AZ237000
DEFINITION RPI-23-7102.TV RPI-23 Mus musculus genomic clone RPI-23-7102,
DNA sequence.
ACCESSION AZ237000
VERSION AZ237000.1 GI:8545046
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus.
REFERENCE 1 (bases 1 to 413)
AUTHORS Zhao, S., Nierman, W., Feldblyum, T., Malek, J., Shatsman, S., Akinret, B., Levins, M., McGann, S., Tsegaye, G., Geer, K., Krol, M., de Jong, P. and Fraser, C.M.
TITLE Mouse BAC End Sequences from Library RPI-23
JOURNAL Unpublished (1999)
COMMENT Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: szhao@tigr.org
Clones are derived from the mouse BAC library RPI-23. For BAC
library availability, please contact Pieter de Jong

```

(pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (<http://bacpac.med.buffalo.edu/orderingframe.htm>) or from Reseach Genetics (http://www.tigr.org/tldb/bac_ends/mouse/bac_end_intro.html). BAC end page: http://www.tigr.org/tldb/bac_ends/mouse/bac_end_intro.html

Plate: 71 row: 0 column: 2
Seq primer: T7
Class: BAC ends.

FEATURES

Location/Qualifiers
source
1..413
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="RPI-23-7102"
/clone_lib="RPI-23"
/sex="Female"
/lab_host="DH10B"
/note="Organ: Kidney/Brain; Vector: pBACE3.6; Site_1: EcoRI; Site_2: EcoRI; Female C57BL/6J mouse kidney and/or brain genomic DNA was isolated and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBACE3.6 vector at the EcoRI sites. The ligation products were transformed into DH10B electrocompetent cells (BRL Life Technologies)."

BASE COUNT 112 a 88 c 78 g 135 t
ORIGIN

alignment_scores:

Quality: 201.00 Length: 86
Ratio: 3.295 Gaps: 4
Percent Similarity: 70.930 Percent Identity: 53.488

alignment_block:

US-09-662-783-4 x AZ237000/rev

Align seg 1/1 to reverse of: AZ237000 from: 1 to: 413

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55 PheProArg.....CysLeuLeuValGlnArgCysGlyAsnCysG1 69
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
379 TTTCCAAGGGTTTACTCACTCATTAACCAAGG..... 347
69 yCysGlyThrValAsnTrpArgSerCysThrCysAsn.SerGlyLysThr 85
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
346 ...GGAATGGGTGAGTGGCATTTGGCTGACTTAATCAAGGGCTTCT 301
86 ValLysLysTyrHisGlu.....ValLeuGlnPheGluPr 97
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
300 AACAGGAATATATCTTCTATCCTTTATTGTAGGTATTGAAGTTTGAGCC 251
97 oGlyHisLysArgArgGlyArgAlaLysThrMetAlaLeuValAspI 114
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
250 TGGACATTTCAAGAGAGAGGCAAGCTAAGATATGCTCTTGTGATA 201
114 leGlnLeuAspHisHisGluArgCysAspCysSerSerArgPro 130
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
200 TCCAGCTGGATCAAAAAGAAAGATGTGACTGTATCTGCAGCTCAAGACCA 151
131 ProArg 132
|||||
150 CCTCGA 145

```


GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 26, 2001, 15:15:09 ; Search time 11.6 Seconds
(without alignments)
389.804 Million cell updates/sec

Title: US-09-662-783-4
Perfect score: 737
Sequence: 1 MYLDPYRGRSYHDKRSKV.....DTQLDHPHRCDCICSSRPR 132

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	100.5	13.6	148	1	VEGH_ORFN7
2	95.5	13.0	188	1	VEGB_MOUSE
3	94	12.8	213	1	PDGA_RABIT
4	93	12.6	419	1	VEGC_HUMAN
5	92	12.5	415	1	VEGC_MOUSE
6	89	12.1	204	1	PDGA_RAT
7	89	12.1	211	1	PDGA_HUMAN
8	89	12.1	211	1	PDGA_MOUSE
9	85.5	11.6	188	1	VEGB_HUMAN
10	84.5	11.5	133	1	VEGH_ORFN2
11	83	11.3	226	1	PDGA_XENLA
12	81	11.0	241	1	PDGB_SHEEP
13	80	10.9	164	1	VEGE_CAVPO
14	79	10.7	241	1	PDGB_MOUSE
15	78	10.6	225	1	PDGB_RAT
16	77	10.4	77	1	MT2_VICFA
17	77	10.4	79	1	MT2_CICAR
18	77	10.4	146	1	VEGE_SHEEP
19	77	10.4	190	1	VEGE_BOVIN
20	77	10.4	245	1	PDGB_FELCA
21	76.5	10.4	1790	1	LMBL_DROME
22	76	10.3	241	1	PDGB_HUMAN
23	74	10.0	77	1	MT1A_VICFA
24	74	10.0	82	1	MT2B_LYCES
25	74	10.0	215	1	VEGE_HUMAN
26	73.5	10.0	82	1	MT2_ORYSA
27	73.5	10.0	158	1	PLGF_MOUSE
28	73	9.9	78	1	MT2_ACTCH
29	73	9.9	79	1	MT2_MALDO
30	73	9.9	170	1	PLGF_HUMAN
31	72	9.8	80	1	MT2_RICCO
32	71	9.6	77	1	MTA_TRIRP
33	71	9.6	78	1	MT2_MUSAC

34	71	9.6	190	1	VEGF_PIG
35	71	9.6	190	1	VEGF_RAT
36	71	9.6	677	1	SP87_DICDI
37	70.5	9.6	75	1	MT1_PEA
38	70.5	9.6	214	1	VEGF_MOUSE
39	70	9.5	80	1	MT2_BRARP
40	70	9.5	81	1	MT2_BRARP
41	70	9.5	81	1	MT2A_ARATH
42	70	9.5	226	1	TSIS_SMSAV
43	69.5	9.4	1069	1	ENTK_MOUSE
44	69	9.4	80	1	MT1_COPAR
45	69	9.4	84	1	MT22_ORYSA

ALIGNMENTS

RESULT 1	VEGH_ORFN7	STANDARD;	PRT;	148 AA.
ID	VEGH_ORFN7			
AC	P52585;			
DT	01-OCT-1996 (Rel. 34, Created)			
DT	01-OCT-1996 (Rel. 34, Last sequence update)			
DE	15-JUL-1999 (Rel. 38, Last annotation update)			
DE	VASCULAR ENDOTHELIAL GROWTH FACTOR HOMOLOG PRECURSOR.			
GN	A2R.			
OS	Orf virus (strain NZ7) (OV NZ-7).			
OC	Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;			
OC	Parapoxvirus.			
OX	NCBI_TaxID=73495;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=94076465; PubMed=8254780;			
RA	Lyttle D.J., Fraser K.M., Fleming S.B., Mercer A.A., Robinson A.J.;			
RT	"Homologs of vascular endothelial growth factor are encoded by the			
RT	poxvirus orf virus.";			
RT	J. Virol. 68:84-92(1994).			
CC	- FUNCTION: INDUCES ENDOTHELIAL PROLIFERATION.			
CC	- SUBUNIT: HOMODIMER, DISULFIDE-LINKED (BY SIMILARITY).			
CC	- SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS.			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
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CC	or send an email to license@isb-sib.ch).			
CC	-----			
CC	EMBL; S67522; AAB29223.1; -			
DR	HSPP; P15692; IVPF.			
DR	InterPro: IPR000072; -			
DR	Pfam; PF00341; PDGF; 1.			
DR	PROSITE; PS00249; PDGF_1; FALSE_NEG.			
DR	PROSITE; PS0278; PDGF_2; 1.			
KW	Mitogen; Growth factor; Glycoprotein; Signal.			
FT	SIGNAL 1 ?			
FT	CHAIN ? 148			
FT	VASCULAR ENDOTHELIAL GROWTH FACTOR			
FT	HOMOLOG.			
FT	DISULFID 46 88			
FT	BY SIMILARITY.			
FT	DISULFID 77 130			
FT	BY SIMILARITY.			
FT	DISULFID 81 132			
FT	BY SIMILARITY.			
FT	DISULFID 71 71			
FT	INTERCHAIN (BY SIMILARITY).			
FT	DISULFID 80 80			
FT	INTERCHAIN (BY SIMILARITY).			
FT	DISULFID 95 95			
FT	N-LINKED (GLCNAC...) (POTENTIAL).			
SQ	SEQUENCE 148 AA; 16078 MW; F0E13BA104CC73F8 CRC64;			

Query Match 13.6%; Score 100.5; DB 1; Length 148;
Best Local Similarity 25.6%; Pred. No. 0.00082;
Matches 32; Conservative 13; Mismatches 31; Indels 49; Gaps 5;
Qy 34 CTPRNSYNIREEL-KLANVVFFRCLLVQRCCGNCG-----CGTVNWRSC----- 79

Db 46 CKPRDTVVYLGEEYDESTNLOYNPCVTKRCGCGNGDQICCTAVETNTTWTVSVCV 105
QY 80 -----CNSGKTVKKYHEVLFQEPGHKRGKRAKTMALVDIQLDHHERCDCI-----CS 127
Db 106 SSSSGTNGSVSTN-----LORISVTEHTKDCICIGRTTTTPT 142
QY 128 SRPPR 132
Db 143 TREPR 147
RESULT 2
VEGB_MOUSE
ID VEGB_MOUSE STANDARD; PRT; 188 AA.
AC P49766;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE VASCULAR ENDOTHELIAL GROWTH FACTOR B PRECURSOR (VEGF-B) (VASCULAR
ENDOTHELIAL GROWTH FACTOR RELATED PROTEIN) (VRF).
GN VEGFB OR VRF.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Heart;
RX MEDLINE=96197355; PubMed=8637916;
RA Olofsson B., Pajusola K., Kaipainen A., von Euler G., Joukov V.,
RA Saksela O., Orpana A., Pattersson R.F., Alitalo K., Eriksson U.,
RT "Vascular endothelial growth factor B, a novel growth factor for
RT endothelial cells."
RL Proc. Natl. Acad. Sci. U.S.A. 93:2576-2581(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=96183052; PubMed=8607868;
RA Townsend S., Lagercrantz J., Grimmond S., Silins G.,
RA Nordenskjöld M., Weber G., Hayward N.K.;
RT "Characterization of the murine VEGF-related factor gene."
RL Biochem. Biophys. Res. Commun. 220:922-928(1996).
CC -!- FUNCTION: GROWTH FACTOR FOR ENDOTHELIAL CELLS. BINDS HEPARIN.
CC -!- SUBUNIT: HOMODIMER, DISULFIDE-LINKED. CAN ALSO FORM HETERODIMER
CC WITH VEGF.
CC -!- SUBCELLULAR LOCATION: SECRETED BUT REMAINS ASSOCIATED TO CELLS OR
CC TO THE EXTRACELLULAR MATRIX UNLESS RELEASED BY HEPARIN.
CC -!- TISSUE SPECIFICITY: ABUNDANTLY EXPRESSED IN HEART, BRAIN, KIDNEY
CC AND SKELETAL MUSCLE.
CC -!- SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS.
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CC
CC EMBL; U48800; AAC06273.1; -
CC EMBL; U43837; AAC52553.1; -
CC HSSP; P15692; 2VGH.
CC MGD; MGI:106199; Vegfb.
CC InterPro: IPR000072; -
CC Pfam; PF00341; PDGF; 1.
CC PROSITE; PS00249; PDGF_1; 1.
CC PROSITE; PS0278; PDGF_2; 1.
CC Mitogen; Growth factor; Signal; Heparin-binding.
FT SIGNAL 1 21 POTENTIAL.
FT CHAIN 22 188 VASCULAR ENDOTHELIAL GROWTH FACTOR B.
SQ SEQUENCE 188 AA; 21442 MW; D52A055F995E9CA CRC64;

Query Match 13.0%; Score 95.5; DB 1; Length 188;
Best Local Similarity 27.9%; Pred No. 0.0035;
Matches 29; Conservative 16; Mismatches 38; Indels 21; Gaps 5;
QY 31 RYSCPTPRNYSVNIREEKLKLVV--FFPRCLLVQRCGNCGGCTVNRSCNCGTKVKK 88
Db 44 RATCOPREVVVPLSMEL-MGNVVKQLVPSCVTVQRCG---GCCPDDGLCEVPTGQHOVRM 99
QY 89 YHEVLFQEPGHKRGKRAKTMALVDIQLDHHERCDCICSSRPPR 132
Db 100 QILMIQY-----PSSQLGEMSEEHQSQC-----RPKK 128
RESULT 3
PDGA_RABIT
ID PDGA_RABIT STANDARD; PRT; 213 AA.
AC P34007;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE PLATELET-DERIVED GROWTH FACTOR, A CHAIN PRECURSOR (PDGF A-CHAIN)
(PDGF-1).
DE (PDGF-1).
GN PDGFA.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Vascular smooth muscle;
RX MEDLINE=92246970; PubMed=1575749;
RA Nakahara K.-I., Nishimura H., Kuro-O M., Takewaki S.-I., Iwase M.,
RA Ohkubo A., Yazaki Y., Nagai R.;
RT "Identification of three types of PDGF-A chain gene transcripts in
RT rabbit vascular smooth muscle and their regulated expression during
RT development and by angiotensin II."
RL Biochem. Biophys. Res. Commun. 184:811-818(1992).
CC -!- FUNCTION: PLATELET-DERIVED GROWTH FACTOR IS A POTENT MITOGEN FOR
CC CELLS OF MESENCHYMAL ORIGIN. BINDING OF THIS GROWTH FACTOR TO ITS
CC AFFINITY RECEPTOR ELICITS A VARIETY OF CELLULAR RESPONSES. IT IS
CC RELEASED BY PLATELETS UPON WOUNDING AND PLAYS AN IMPORTANT ROLE
CC IN STIMULATING ADJACENT CELLS TO GROW AND THEREBY HEAL THE WOUND.
CC -!- SUBUNIT: ANTIPARALLEL DISULFIDE-LINKED DIMER OF NONIDENTICAL (A
CC AND B) CHAINS. HOMODIMERS OF A AND B CHAINS ARE IMPLICATED IN
CC TRANSFORMATION PROCESSES.
CC -!- ALTERNATIVE PRODUCTS: 3 ISOFORMS; A1, A2 (SHOWN HERE) AND A3; ARE
CC PRODUCED BY ALTERNATIVE SPLICING.
CC -!- INDUCTION: THE FORM A3 IS SELECTIVELY INDUCED BY ANGIOTENSIN II.
CC -!- MISCELLANEOUS: A-A AND B-B, AS WELL AS A-B, DIMERS CAN BIND TO THE
CC PDGF RECEPTOR.
CC -!- SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS.
CC PIR; JS0735; JS0735.
CC PIR; JS0387; PS0387.
CC PIR; JN0248; JN0248.
CC HSSP; P01127; 1PDG.
CC InterPro: IPR000072; -
CC InterPro: IPR002400; -
CC Pfam; PF00341; PDGF; 1.
CC PRINTS; PR00438; GFCYSKNOT.
CC PROSITE; PS00249; PDGF_1; 1.
CC PROSITE; PS0278; PDGF_2; 1.
CC Glycoprotein; Mitogen; Growth factor; Platelet; Alternative splicing;
CC Signal. 1 20
CC SIGNAL 21 89 BY SIMILARITY.
CC PROPEP 21 89 REMOVED BY PROTEOLYSIS (BY SIMILARITY).
CC CHAIN 90 213 PLATELET-DERIVED GROWTH FACTOR, A CHAIN.
CC SITE 158 162 RECEPTOR BINDING SITE (POTENTIAL).
CC DISULFID 131 179 BY SIMILARITY.
CC DISULFID 135 181 BY SIMILARITY.
CC DISULFID 125 125 INTERCHAIN (BY SIMILARITY).
CC DISULFID 134 134 INTERCHAIN (BY SIMILARITY).
CC CARBOHYD 136 136 N-LINKED (GLCNAC...) (POTENTIAL).


```
FT VARSPLIC 196 198 GRR -> DVR (IN ISOFORM A1).
FT VARSPLIC 199 213 MISSING (IN ISOFORM A1).
FT VARSPLIC 197 213 RRESGKKRRKRLRPT -> TLLPAPGVHPOGCLRAHDG
FT VARSPLIC 197 213 COSSRNHMOALGWKKM (IN ISOFORM A3).
SQ SEQUENCE 213 AA; 24005 MW; 28A9B7E50487F4C5 CRC64;

Query Match 12.8%; Score 94; DB 1; Length 213;
Best Local Similarity 28.0%; Pred. No. 0.0058;
Matches 23; Conservative 17; Mismatches 32; Indels 10; Gaps 3;

QY 50 ANVVFPRCLLVQRCGCGTWNRSCTCNSGKTWKYHEVLOFEPGHKIKRGRAKTM 109
|| : || : || : || : || : || : || : || : || : || : || : || : ||
Db 117 ANFLWPPCVVEVKCTGCC-----NTSSVKQCPSRVHRSYKVAKE--YVRKKPKLKE- 168
|| : || : || : || : || : || : || : || : || : || : || : || : ||

QY 110 ALVDIQLDHERCDICSSRPP 131
|| : || : || : || : || : || : || : || : || : || : || : || : ||
Db 169 --VQVRLEEHLECAASSAGP 188

RESULT 4
VEGC_HUMAN STANDARD; PRT; 419 AA.
AC P49767;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE VASCULAR ENDOTHELIAL GROWTH FACTOR C PRECURSOR (VEGF-C) (VASCULAR
DE ENDOTHELIAL GROWTH FACTOR RELATED PROTEIN) (VRP) (FLT4 LIGAND) (FLT4-
DE L).
GN VEGFC.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 103-120.
RX MEDLINE=96178224; PubMed=8617204;
RA Joukov V., Pajusola K., Kaipainen A., Chilov D., Lahtinen I., Kukk E.,
RA Saksela O., Kalkkinen N., Alitalo K.;
RA "A novel vascular endothelial growth factor, VEGF-C, is a ligand for
RT the Flt4 (VEGFR-3) and KDR (VEGFR-2) receptor tyrosine kinases.";
RL EMBO J. 15:290-298(1996).
RN [2]
RP ERRATUM.
RX MEDLINE=96203094; PubMed=8612600;
RA Joukov V., Pajusola K., Kaipainen A., Chilov D., Lahtinen I., Kukk E.,
RA Saksela O., Kalkkinen N., Alitalo K.;
RL EMBO J. 15:1751-1751(1996).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=96312526; PubMed=8700872;
RA Lee J., Gray A., Yuan J., Luoh S.-M., Avraham H., Wood W.I.;
RA "Vascular endothelial growth factor-related protein: a ligand and
RT specific activator of the tyrosine kinase receptor Flt4.";
RL Proc. Natl. Acad. Sci. U.S.A. 93:1988-1992(1996).
RN [4]
RP SEQUENCE FROM N.A.
RA Fitz L., Morris J.C., Towler P.S., Long A.J., Greco R.,
RA Burgess P., Giannotti J., Ciarletta A., Hennessey D., Kovacic S.,
RA Fitzgerald M., Scaltreto H., Welch N., Neben S., Finnerty H.,
RA Zollner R., Wang J., Nickbarg E., Gassaway R., Turner K.,
RA Wood C.R.;
RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: GROWTH FACTOR ACTIVE IN ANGIOGENESIS, AND ENDOTHELIAL
CC CELL GROWTH.
CC -!- SUBUNIT: HOMODIMER, DISULFIDE-LINKED.
CC -!- PTM: PROBABLY PROTEOLITICALLY PROCESSED IN THE C-TERMINUS.
CC -!- SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS.
CC -----
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CC -----
CC EMBL; X94216; CAA63907.1; -
CC EMBL; U43142; AAA85214.1; -
CC EMBL; U58111; AAB02909.1; -
CC HSSP; P15692; 1VPF.
CC MIM; 601528; -
CC InterPro; IPR000072; -
CC InterPro; IPR002400; -
CC Pfam; PF00341; PDGF; 1.
CC PRINTS; PR00438; GFCYSKNOT.
CC PROSITE; PS00249; PDGF_1; 1.
CC PROSITE; PS00278; PDGF_2; 1.
CC Mitogen; Growth factor; Glycoprotein; Signal; Repeat.
KW SIGNAL 1
FT PROPEP ? 102
FT CHAIN 103 419 VASCULAR ENDOTHELIAL GROWTH FACTOR C.
FT DOMAIN 275 365 4 X 24 AA TANDEM REPEATS.
FT REPEAT 275 298 1.
FT REPEAT 299 322 2.
FT REPEAT 323 346 3.
FT REPEAT 347 365 4 (PARTIAL).
FT CARBOHYD 175 175 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 205 205 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 240 240 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 419 AA; 46883 MW; 9F598719DB3E014F CRC64;

Query Match 12.6%; Score 93; DB 1; Length 419;
Best Local Similarity 20.7%; Pred. No. 0.015;
Matches 38; Conservative 20; Mismatches 50; Indels 76; Gaps 8;

QY 22 LDRLNDDAKRYSCTPRNYSVNIREELKLANVVF-PRCLLVORCGNGC----- 69
| : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : |
Db 119 LKSIDNEWRKTCQMPREVCIDVGKEFGVATNTEFKPCVSVYRGCGCGNSEGQCMTST 178
| : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : |
QY 70 -----CGTVNWRSCNCSGKTV-KKYHEVLQ----- 94
| : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : |
Db 179 SYLSKTLFEITVPLSQGPKVPTISFANTHSCRCMSKLDVYQVHVSIRSLPATLPQCQA 238
| : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : |
QY 95 -----FEPGHKIR-----RGRAKTMALVDI-----QLDHHRCDCICSS 128
| : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : |
Db 239 ANKTCPTNYMWNHICRCLAQEDFWSDDAGDSTDGFDHICGPNKELD-BETCQCVCRA 297
| : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : |
QY 129 --RP 130
| : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : |
Db 298 GLRP 301

RESULT 5
VEGC_MOUSE STANDARD; PRT; 415 AA.
AC P97953;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE VASCULAR ENDOTHELIAL GROWTH FACTOR C PRECURSOR (VEGF-C) (FLT4 LIGAND)
DE (FLT4-L).
GN VEGFC.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C;
RA MEDLINE=97164697; PubMed=9012504;
RA Kukk E., Lymboussaki A., Taira S., Kaipainen A., Jeltsch M.,
RA Joukov V., Alitalo K.;
RT "VEGF-C receptor binding and pattern of expression with VEGFR-3
```

RT suggests a role in lymphatic vascular development.";

RL Development 122:3829-3837(1996).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=BALE/C;

RX MEDLINE=97388482; PubMed=9247316;

RA Fitz L.J., Morris J.C., Towler P., Long A., Burgess P., Greco R.,

RA Wang J., Gassaway R., Nickbarg E., Kovacic S., Ciarletta A.,

RA Giannotti J., Finnerty H., Zollner R., Beier D.R., Leak L.V.,

RA Turner K.J., Wood C.R.;

RT "Characterization of murine Flt4 ligand/VEGF-C.";

RL Oncogene 15:613-618(1997).

CC -!- FUNCTION: GROWTH FACTOR ACTIVE IN ANGIOGENESIS, AND ENDOTHELIAL

CC CELL GROWTH.

CC -!- SUBUNIT: HOMODIMER, DISULFIDE-LINKED (BY SIMILARITY).

CC -!- SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS.

CC -----

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CC -----

DR EMBL; U73620; AAC52984.1; -;

DR EMBL; U58112; AAB46707.1; -;

DR HSSP; P15692; 1VPF.

DR MGD; MGI:109124; Vegfc.

DR InterPro; IPR000072; -;

DR InterPro; IPR002400; -;

DR Pfam; PF00341; PDGF; 1.

DR PRINTS; PR00438; GFCYSKNOT.

DR PROSITE; PS00249; PDGF.1; 1.

DR PROSITE; PS50278; PDGF.2; 1.

KW Mitogen; Growth factor; Glycoprotein; Signal; Repeat.

FT SIGNAL 1 ?

FT PROPEP ? 98

FT CHAIN 99 415

FT DOMAIN 271 361

FT REPEAT 271 294

FT REPEAT 295 318

FT REPEAT 319 342

FT REPEAT 343 361

FT CARBOHYD 171 171

FT CARBOHYD 201 201

FT CARBOHYD 236 236

SQ SEQUENCE 415 AA; 46471 MW; D9D3DD3CECC659D6 CRC64;

Query Match 12.5%; Score 92; DB 1; Length 415;

Best Local Similarity 24.3%; Pred. No. 0.019;

Matches 27; Conservative 18; Mismatches 42; Indels 24; Gaps 4;

QY 22 LDRLNDKAKRYCTPRNYSVNTRREELKLANVVF-PRCLLVRCGNCGCCGVNWRSC7C 80

| : : : : | | | : : | | | : | | | |

Db 115 LKSIDNEWKTCQMPREVCIDVKGEGAAITFFKPCVSVYRCGCC-----NSEGLQC 169

QY 81 NSGKTVKKYHEVLQFPFGHKRGRKAKTAL-----VDIQLDHHERCDCI 125

| : : : : | : : | : | : | : |

Db 170 MNTST-----GYLSKTLFEITVPLSQGPKPVTVISFANHTSCRM 208

RESULT 6

PDGA_RAT

ID PDGA_RAT

AC P28576; STANDARD; PRT; 204 AA.

DT 01-DEC-1992 (Rel. 24, Created)

DT 01-FEB-1994 (Rel. 28, Last sequence update)

DT 01-OCT-2000 (Rel. 40, Last annotation update)

DE PLATELET-DERIVED GROWTH FACTOR, A CHAIN PRECURSOR (PDGF A-CHAIN)

DE (PDGF-1).

GN PDGPA OR RPAL.

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCBI_TaxID=10116;

RN [1]

RP SEQUENCE OF 8-204 FROM N.A.

RX MEDLINE=93305723; PubMed=8318539;

RA Herren B., Weyer K.A., Rouge M., Loetscher P., Pech M.;

RT "Conservation in sequence and affinity of human and rodent PDGF

RT ligands and receptors.";

RL Biochim. Biophys. Acta 1173:294-302(1993).

RN [2]

RP SEQUENCE FROM N.A.

RX MEDLINE=93191115; PubMed=8447423;

RA Katayose D., Ohe M., Yamauchi K., Ogata M., Shirato K., Fujita H.,

RA Shibahara S., Takishima T.;

RT "Increased expression of PDGF A- and B-chain genes in rat lungs with

RT hypoxic pulmonary hypertension.";

RL Am. J. Physiol. 264:L100-L106(1993).

RN [3]

RP SEQUENCE FROM N.A. (SHORT FORM).

RA Xia Y., Feng L., Tang W.W., Wilson C.B.;

RT "Cloning and expression of rat platelet-derived growth factor

RT A-chain.";

RL J. Am. Soc. Nephrol. 3:622-622(1992).

RN [4]

RP SEQUENCE OF 58-196 FROM N.A. (SHORT FORM).

RC STRAIN=FISCHER 344; TISSUE=Smooth muscle;

RX MEDLINE=93225589; PubMed=8469035;

RA Szabo P., Wexler D., Whittington E., Wexler B.B.;

RT "The age-dependent proliferation of rat aortic smooth muscle cells is

RT independent of differential splicing of PDGF A-chain mRNA.";

RL Mech. Ageing Dev. 67:79-89(1993).

CC -!- FUNCTION: PLATELET-DERIVED GROWTH FACTOR IS A POTENT MITOGEN FOR

CC CELLS OF MESENCHYMAL ORIGIN. BINDING OF THIS GROWTH FACTOR TO ITS

CC AFFINITY RECEPTOR ELICITS A VARIETY OF CELLULAR RESPONSES. IT IS

CC RELEASED BY PLATELETS UPON WOUNDING AND PLAYS AN IMPORTANT ROLE

CC IN STIMULATING ADJACENT CELLS TO GROW AND THEREBY HEAL THE WOUND.

CC -!- SUBUNIT: ANTIPARALLEL DISULFIDE-LINKED DIMER OF NONIDENTICAL (A

CC AND B) CHAINS. HOMODIMERS OF A AND B CHAINS ARE IMPLICATED IN

CC TRANSFORMATION PROCESSES.

CC -!- ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE) AND A

CC SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPLICING. THE LONG FORM

CC CONTAINS A BASIC INSERT WHICH ACTS AS A CELL RETENTION SIGNAL.

CC -!- DEVELOPMENTAL STAGE: IN KIDNEY EPITHELIAL TISSUES, THE SHORTER

CC FORM PREDOMINATES IN YOUNG (1 DAY OLD) RATS WHILE THE LONGER FORM

CC BECOMES MORE PREVALENT DURING AGING.

CC -!- MISCELLANEOUS: A-A AND B-B, AS WELL AS A-B, DIMERS CAN BIND TO THE

CC PDGF RECEPTOR.

CC -!- SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS.

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CC or send an email to license@isb-sib.ch).

CC -----

DR EMBL; L06894; AAB59693.1; -;

DR EMBL; Z14120; CAA78490.1; -;

DR EMBL; D10106; BAA00987.1; -;

DR EMBL; L06238; AAA1932.1; -;

DR EMBL; S57864; AAB26134.2; -;

DR HSSP; P01127; 1PDG.

DR InterPro; IPR000072; -;

DR InterPro; IPR002400; -;

DR Pfam; PF00341; PDGF; 1.

DR PRINTS; PR00438; GFCYSKNOT.

DR PROSITE; PS00249; PDGF.1; 1.

DR PROSITE; PS50278; PDGF.2; 1.

KW Glycoprotein; Mitogen; Growth factor; Platelet; Alternative splicing;

KW Signal.

FT SIGNAL 1 20 BY SIMILARITY.
FT PROPEP 21 85 REMOVED BY PROTEOLYSIS.
FT CHAIN 86 204 PLATELET-DERIVED GROWTH FACTOR, A CHAIN.
FT SITE 158 162 RECEPTOR BINDING SITE (POTENTIAL).
FT DISULFID 96 140 BY SIMILARITY.
FT DISULFID 129 177 BY SIMILARITY.
FT DISULFID 133 179 BY SIMILARITY.
FT DISULFID 123 123 INTERCHAIN (BY SIMILARITY).
FT DISULFID 132 132 INTERCHAIN (BY SIMILARITY).
FT CARBOHYD 134 134 N-LINKED (GLCNAC...) (BY SIMILARITY).
FT VARSPLIC 194 204 GRR -> DVR (IN SHORT ISOFORM).
FT VARSPLIC 197 204 MISSING (IN SHORT ISOFORM).
FT CONFLICT 85 111 KRSEEAIPAVCKTRTVIPIRSQVD -> REVLKPPFPQ
FT CONFLICT 119 119 FAPGRSFTYLGARWT (IN REF. 2).
FT CONFLICT 204 AA; 23307 MW; FA413F74E86F742C CRC64;
FT SEQUENCE 204 AA; 23307 MW; FA413F74E86F742C CRC64;
FT SEQUENCE 204 AA; 23307 MW; FA413F74E86F742C CRC64;
Query Match 12.1%; Score 89; DB 1; Length 204;
Best Local Similarity 26.8%; Pred. No. 0.019;
Matches 22; Conservative 18; Mismatches 32; Indels 10; Gaps 3;
QY 50 ANVVEFFCLLVQRCGGCGTWNWSCITCNCKTVKKYHEVLQFPGCHKRGRKATM 109
Db 115 ANFLWPPCVVEKRTGCTCC-----NTSSVKQCPQSRVHRHRSYKVKAVE--YVRRKKPKLKE- 166
QY 110 ALVDIQLDHHRCDCICSSRPP 131
Db 167 --VQVRLEEHLECAVSNLNP 186
RESULT 7
PDGA_HUMAN STANDARD; PRT; 211 AA.
AC P04085;
DT 01-NOV-1986 (Rel. 03, Created)
DT 01-NOV-1986 (Rel. 03, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE PLATELET-DERIVED GROWTH FACTOR, A CHAIN PRECURSOR (PDGF A-CHAIN)
DE (PDGF-1).
GN PDGFA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=8814463; PubMed=3422746;
RA Bonthron D.T., Morton C.C., Orkin S.H., Collins T.;
RT "Platelet-derived growth factor A chain: gene structure, chromosomal location, and basis for alternative mRNA splicing";
RL Proc. Natl. Acad. Sci. U.S.A. 85:1492-1496(1988).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=8817469; PubMed=2832727;
RA Rorsman F., Bywater M., Knott T.J., Scott J., Betsholtz C.;
RT "Structural characterization of the human platelet-derived growth factor A-chain cDNA and gene: alternative exon usage predicts two different precursor proteins";
RL Mol. Cell. Biol. 8:571-577(1988).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=86203630; PubMed=3754619;
RA Betsholtz C., Johansson A., Heldin C.H., Westermark B., Lind P.,
RA Urdea M.S., Eddy R., Shows T.B., Philpott K., Mellor A.L., Knott T.J.,
RA Scott J.;
RT "cDNA sequence and chromosomal localization of human platelet-derived growth factor A-chain and its expression in tumour cell lines";
RL Nature 320:695-699(1986).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=88030061; PubMed=3666150;
RA Hoppe J., Schumacher L., Eichner W., Weich H.A.;
RT "The long 3'-untranslated regions of the PDGF-A and -B mRNAs are only distantly related";
RL FEBS Lett. 223:243-246(1987).
RN [5]
RP SEQUENCE OF 1-53 FROM N.A.
RX MEDLINE=93252628; PubMed=8486521;
RA Takimoto Y., Li W.Y., Wang Z.Y., Tong B.D., Deuel T.F.;
RT "Nucleotide sequence of the 5' region of the human platelet-derived growth factor A-chain gene";
RL Hiroshima J. Med. Sci. 42:47-52(1993).
RN [6]
RP ALTERNATIVE SPLICING.
RX MEDLINE=87287247; PubMed=3614363;
RA Tong B.D., Auer D.E., Jaye M., Kaplow J.M., Ricca G., McConathy E.,
RA Drohan W., Deuel T.F.;
RT "cDNA clones reveal differences between human glial and endothelial cell platelet-derived growth factor A-chains";
RL Nature 328:619-621(1987).
RN [7]
RP ALTERNATIVE SPLICING.
RX MEDLINE=87287248; PubMed=3614364;
RA Collins T., Bonthron D.T., Orkin S.H.;
RT "Alternative RNA splicing affects function of encoded platelet-derived growth factor A chain";
RL Nature 328:621-624(1987).
RN [8]
RP INTERCHAIN DISULFIDE BONDS.
RX MEDLINE=92283833; PubMed=1317862;
RA Andersson M., Oestman A., Baekstroem G., Hellman U.,
RA George-Nascimento C., Westmark B., Heldin C.-H.;
RT "Assignment of interchain disulfide bonds in platelet-derived growth factor (PDGF) and evidence for agonist activity of monomeric PDGF";
RL J. Biol. Chem. 267:11260-11266(1992).
CC -!- FUNCTION: PLATELET-DERIVED GROWTH FACTOR IS A POTENT MITOGEN FOR CELLS OF MESENCHYMAL ORIGIN. BINDING OF THIS GROWTH FACTOR TO ITS AFFINITY RECEPTOR ELICITS A VARIETY OF CELLULAR RESPONSES. IT IS RELEASED BY PLATELETS UPON WOUNDING AND PLAYS AN IMPORTANT ROLE IN STIMULATING ADJACENT CELLS TO GROW AND THEREBY HEAL THE WOUND.
CC -!- SUBUNIT: ANTIPARALLEL DISULFIDE-LINKED DIMER OF NONIDENTICAL (A AND B) CHAINS. HOMODIMERS OF A AND B CHAINS ARE IMPLICATED IN TRANSFORMATION PROCESSES.
CC -!- ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE) AND A SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPLICING. THE LONG FORM CONTAINS A BASIC INSERT WHICH ACTS AS A CELL RETENTION SIGNAL.
CC -!- MISCELLANEOUS: A-A AND B-B, AS WELL AS A-B, DIMERS CAN BIND TO THE PDGF RECEPTOR.
CC -!- SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS.
CC -!- DATABASE: NAME-R&D Systems' cytokine source book; WWW="http://www.rndsystems.com/cyt_cat/pdgm.html".
CC -----
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CC -----
DR EMBL; M21571; -; NOT_ANNOTATED_CDS.
DR EMBL; X03795; CAA27421.1; -;
DR EMBL; X06374; CAA29677.1; -;
DR EMBL; M20494; AAA60045.1; -;
DR EMBL; M20488; AAA60045.1; JOINED.
DR EMBL; M20489; AAA60045.1; JOINED.
DR EMBL; M20490; AAA60045.1; JOINED.
DR EMBL; M20491; AAA60045.1; JOINED.
DR EMBL; M20492; AAA60045.1; JOINED.
DR EMBL; M20493; AAA60045.1; JOINED.
DR EMBL; M19988; AAA60046.1; -;
DR EMBL; M21571; AAA60046.1; JOINED.
DR EMBL; M19984; AAA60046.1; JOINED.
DR EMBL; M19985; AAA60046.1; JOINED.
DR EMBL; M19986; AAA60046.1; JOINED.


```

DR InterPro: IPR002400; -
DR Pfam: PF00341; PDGF_1.
DR PRINTS: PR00438; GFCYSKNOT.
DR PROSITE: PS00249; PDGF_1; 1.
DR PROSITE: PS0278; PDGF_2; 1.
DR Glycoprotein; Mitogen; Growth factor; Platelet; Alternative splicing;
KW Signal.
KW SIGNAL.
FT 1 22 REMOVED BY PROTEOLYSIS.
FT PROPEP 23 91 PLATELET-DERIVED GROWTH FACTOR, A CHAIN.
FT CHAIN 92 226 BY SIMILARITY.
FT DISULFID 101 145 BY SIMILARITY.
FT DISULFID 134 182 BY SIMILARITY.
FT DISULFID 138 184 BY SIMILARITY.
FT DISULFID 128 128 INTERCHAIN (BY SIMILARITY).
FT DISULFID 137 137 INTERCHAIN (BY SIMILARITY).
FT CARBOHYD 139 139 N-LINKED (GLCNAC. .) (PROBABLE).
FT VARSPPLIC 198 200 GFF -> DVR (IN SHORT ISOFORM).
FT VARSPPLIC 201 226 MISSING (IN SHORT ISOFORM).
FT CONFLICT 199 209 MISSING (IN REF. 2).
FT CONFLICT 218 218 O -> R (IN REF. 2).
FT SEQUENCE 226 AA; 25719 MW; E3E724FCF67C2FB2 CRC64;

Query Match 11.3%; Score 83; DB 1; Length 226;
Best Local Similarity 26.6%; Pred. No. 0.09;
Matches 21; Conservative 18; Mismatches 30; Indels 10; Gaps

QY 50 ANVVFFRCLLVORCGNCCGTVNRSTCNSGKTVKYKHYEVLQEPGHKRRGAKTM 109
| | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 120 ANFLWPPCPVEVRKTCGCC-----NTSSVKQPSRIHRSVKVAKVE--YVRKKPKLKE- 171
| | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 110 ALVDIQLDHRHCDCICSS 128
| | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 172 --VLVRL EEHLECTCTANS 188
| | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

RESULT 12
PDGB_SHEEP STANDARD; PRT; 241 AA.
ID AC PDGB_SHEEP STANDARD; PRT; 241 AA.
IC AC Q95229;
DT DT 01-NOV-1997 (Rel. 35, Created)
DT DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE DE PLATELET-DERIVED GROWTH FACTOR, B CHAIN PRECURSOR (PDGF B-CHAIN)
DE DE (PDGF-2).
GS GS PDGB.
OS OS Ovis aries (Sheep).
OC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC OC Bovidae; Caprinae; Ovis.
OX OX NCBI_Taxid=9940;
RN RN [1]
RP RP SEQUENCE FROM N.A.
RC RC STRAIN=TEXEL; TISSUE=Spleen;
RA RA Woodall C.J., Zhang Z., Watt N.J.;
RL RL Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.
CC CC -! FUNCTION: PLATELET-DERIVED GROWTH FACTOR IS A POTENT MITOGEN FOR
CC CC CELLS OF MESENCHYMAL ORIGIN. BINDING OF THIS GROWTH FACTOR TO ITS
CC CC AFFINITY RECEPTOR ELICITS A VARIETY OF CELLULAR RESPONSES. IT IS
CC CC RELEASED BY PLATELETS UPON WOUNDING AND PLAYS AN IMPORTANT ROLE
CC CC IN STIMULATING ADJACENT CELLS TO GROW AND THEREBY HEAL THE WOUND.
CC CC -! SUBUNIT: ANTI-PAALLEL DISULFIDE-LINKED DIMER OF NONIDENTICAL (A
CC CC AND B) CHAINS. HOMODIMERS OF A AND B CHAINS ARE IMPLICATED IN
CC CC TRANSFORMATION PROCESSES.
CC CC -! MISCELLANEOUS: A-A AND B-B, AS WELL AS A-B, DIMERS CAN BIND TO THE
CC CC PDGF RECEPTOR.
CC CC -! SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS.
-----
CC CC This SWISS-PROT entry is copyright. It is produced through a collabor
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CC CC use by non-profit institutions as long as its content is in no way
CC CC modified and this statement is not removed. Usage by and for comm
CC CC

```


Search completed: September 26, 2001, 15:16:36
Job time: 87 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 26, 2001, 15:15:09 ; Search time 14.39 Seconds
(without alignments)
698.752 Million cell updates/sec

Title: US-09-662-783-4
Perfect score: 737
Sequence: 1 MYLDPYRGGRSYHDKRSKV.....DIQLDHHERCDCICSRPRP 132

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- PIR_68.*
- 1: pir1.*
- 2: pir2.*
- 3: pir3.*
- 4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	100.5	13.6	148	2 D49530	16K vascular endot
2	95.5	13.0	188	2 JC4680	vascular endothe
3	95.5	13.0	207	2 JC4679	vascular endothe
4	94	12.8	166	2 JN0248	platelet-derived g
5	94	12.8	198	2 JS0735	platelet-derived g
6	93	12.6	419	2 S69207	vascular endothe
7	89	12.1	196	2 A37359	platelet-derived g
8	89	12.1	196	2 B28964	platelet-derived g
9	89	12.1	196	2 A48851	platelet-derived g
10	89	12.1	197	2 S25096	platelet-derived g
11	89	12.1	211	1 PFHUG1	platelet-derived g
12	84.5	11.5	133	2 B49530	vascular endothe
13	83.5	11.3	80	2 T03404	metallothionein-li
14	83	11.3	200	2 T51551	platelet-derived g
15	83	11.3	215	2 S08220	platelet-derived g
16	83	11.3	226	2 T51550	platelet-derived g
17	79	10.7	241	1 PFMSG8	metallothionein-li
18	78.5	10.7	80	2 T02063	epidermal growth f
19	78.5	10.7	333	2 B45558	epidermal growth f
20	78.5	10.7	342	2 C45558	epidermal growth f
21	78.5	10.7	366	2 A45558	epidermal growth f
22	78.5	10.7	1717	1 S25097	platelet-derived g
23	78	10.6	225	2 G71265	hypothetical prote
24	78	10.6	297	2 G71265	metallothionein -
25	77	10.4	77	2 S52636	vascular endothe
26	77	10.4	120	2 A33787	ovine vascular end
27	77	10.4	146	2 S57956	vascular endothe
28	77	10.4	190	2 B40080	platelet-derived g
29	77	10.4	245	1 TVCTSS	platelet-derived g

ALIGNMENTS

RESULT 1

D49530

16K vascular endothelial growth factor homolog A2R - Orf virus

C:Species: Orf virus

C:Date: 07-Apr-1994 #sequence_revision 18-Nov-1994 #text_change 08-Oct-1999

C:Accession: D49530

R:Lyttle, D.J.; Fraser, K.M.; Fleming, S.B.; Mercer, A.A.; Robinson, A.J.

J. Virol. 68, 84-92, 1994

A:Title: Homologs of vascular endothelial growth factor are encoded by the poxvirus o

A:Reference number: A49530; MUID:94076465

A:Contents: N27

A:Accession: D49530

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-148 <LYT>

A:Cross-references: GB:S67522; NID:g456900; PIDN:AAB2923.1; PID:g456902

A:Note: sequence extracted from NCBI backbone (NCBIN:141422, NCBIPI:141426)

Query Match 13.6%; Score 100.5; DB 2; Length 148;

Best Local Similarity 25.6%; Pred. No. 0.0055;

Matches 32; Conservative 13; Mismatches 31; Indels 49; Gaps 5;

Qy 34 CTPRNYSNIREEL-KLANVVFPPCLLVQRCGNGC-----CGTVNWRSC----- 79

Db 46 CKPRDTVVYLGEYEPSTNLOYNPRCVTKRCSCGCGGQICTAVERNTTVVSVTVGV 105

Qy 80 -----CNSGKTVKKYHEVLQFEPGHIKRRGRAKTMALVDIQLDHHERCDCI-----CS 127

Db 106 SSSSCTNSGVSTN-----LQRISVTEHTKDCICGRTTTTPTT 142

Qy 128 SRPRP 132

Db 143 TREPR 147

RESULT 2

JC4680

vascular endothelial growth factor-related factor 167 precursor - mouse

N:Alternate names: VRF 167 protein

C:Species: Mus musculus (house mouse)

C:Date: 10-May-1996 #sequence_revision 19-Jul-1996 #text_change 05-Nov-1999

C:Accession: JC4680

R:Townson, S.; Lagercrantz, J.; Grimmond, S.; Silins, G.; Nordenskjold, M.; Weber, G

Biochem. Biophys. Res. Commun. 220, 922-928, 1996

A:Title: Characterization of the murine VEGF-related factor gene.

A:Reference number: JC4679; MUID:96183052

A:Accession: JC4680

A:Molecule type: mRNA

A:Residues: 1-188 <TOM>

A:Cross-references: GB:U43837; NID:gl314335; PIDN:AAC52553.1; PID:gl314336

C:Comment: This factor is a mitogen, that is selective for endothelial cells, and bel

A;Reference number: S61795; MUID:96178224
A;Accession: S61795
A;Status: nucleic acid sequence not shown; not compared with conceptual translation
A:Molecule type: mRNA
A;Residues: 70-419 <JOU1>
A;Note: this sequence has been revised in reference S69207
A;Accession: S71443
A:Molecule type: protein
A;Residues: 'X',104-120 <JOU2>
R;Lee, J.; Gray, A.; Yuan, J.; Luoh, S.M.; Avraham, H.; Wood, W.I.
submitted to the EMBL Data Library, December 1995
A;Description: Vascular endothelial growth factor related protein (VRP): A ligand and se
A;Reference number: S69208
A;Accession: S69208
A:Molecule type: mRNA
A;Residues: 1-419 <LEE>
A;Cross-references: EMBL:U43142; NID:g1150988; PIDN:AAA85214.1; PID:g1150989
R;Morris, J.C.
submitted to the EMBL Data Library, May 1996
A;Reference number: H01557
A;Accession: G02659
A;Status: preliminary; translated from GB/EMBL/DDBY
A:Molecule type: mRNA
A;Residues: 1-419 <WOR>
A;Cross-references: EMBL:U58111; NID:g1373426; PIDN:AAB02909.1; PID:g1373427
C;Genetics:
A;Gene: GDB:VEGFC; VRP
A;Cross-references: GDB:3890883; OMIM:601528
F;1-12/Domain: signal sequence #status predicted <SIG>
F;13-102/Domain: propeptide #status predicted <PRO>
F;103-419/Product: vascular endothelial growth factor C #status experimental <MAT>

Query Match 12.6%; Score 93; DB 2; Length 419;
Best Local Similarity 20.7%; Pred.No. 0.085;
Matches 38; Conservative 20; Mismatches 50; Indels 76; Gaps 8;

QY : 22 LDRLLDAKRYSCTPRNYSVNIREELKANVVF--PRCLLVQRGGNGC----- 69
| ::::: | | | | | | | | | | | | | | |
Db 119 LKSIDNEWRKTQCMPREVCIDVGKEFGVATNTFFKPCVSIVRCGCCNSEGLQCMNTST 178

QY - 70 -----CGTVNRWRSCTNSGTIV-KKYHEVLQ----- 94
| | | | | | | | | | | | | | |
Db 179 SYLSKTLFEITVPLSQGPKPVTISFANHTSCRCKSLDVYRVHSHIIRSLPATLPQQA 238

QY 95 -----PEPGHKR-----RGRAKTMALVDI-----OLDHERDCICSS 128
| | | | | | | | | | | | | | |
Db 239 ANKTCPTNYMNNHICRLAQEDPFMFSSDGDSTDGFHDICGNPKELD-EETCCVCRA 297

QY 129 --RP 130
||
Db 298 GLRP 301

RESULT 7
A37359
platelet-derived growth factor chain A precursor - mouse
C:Species: Mus musculus (house mouse)
C>Date: 19-Mar-1993 #sequence_revision 19-Mar-1993 #text_change 07-May-1999
C;Accession: A37359
R;Mercola, M.; Wang, C.; Kelly, J.; Brownlee, C.; Jackson-Grusby, L.; Stiles, C.; Bowen
Dev. Biol. 138, 114-122, 1990
A;Title: Selective expression of PDGF A and its receptor during early mouse embryogenesis
A;Reference number: A37359; MUID:90169294
A;Accession: A37359
A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra
A:Molecule type: mRNA
A;Residues: 1-196 <MER>
A;Cross-references: GB:M29464
C;Superfamily: platelet-derived growth factor

Query Match 12.1%; Score 89; DB 2; Length 196;

Best Local Similarity 26.8%; Pred. No. 0.1; Gaps 3;
Matches 22; Conservative 18; Mismatches 32; Indels 10;

QY 50 ANVVFPCLLIVQRGCGGTWNWRSCTCNSKTKVKKYHEVLQFPFGHIKRGRAKTM 109
| : | : | : | : | : | : | : | : | : | : | : | : |
Db 115 ANFLWPCEVEKRGTCGCC-----NTSSVKQPISRHHRSVKVAKE--YVRKKPKLKE- 166

QY 110 ALVDIQLDHHERCDCICSSRRP 131
| : | : | : | : | : | : | : | : | : | : | : | : |
Db 167 --VVRLLEHLECACATSLNP 186

RESULT 8
B28964 platelet-derived growth factor chain A precursor splice form 2 - human
C:Species: Homo sapiens (man)
C>Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 16-Jul-1999
C:Accession: B28964; B42002; B28122 R:Bonthron, D.T.; Morton, C.C.; Orkin, S.H.; Collins, T.
Proc. Natl. Acad. Sci. U.S.A. 85, 1492-1496, 1988
A>Title: Platelet-derived growth factor A chain: gene structure, chromosomal location
A:Reference number: A28964; MUID:88144463
A:Accession: B28964
A:Molecule type: DNA
A:Residues: 1-196 <BON>
A:CROSS-references: GB:M21571; GB:J03638; GB:M1984; GB:M1985; GB:M1986; GB:M1987;
R:Bonthron, D.; Collins, T.; Grzeschik, K.H.; van Roy, N.; Speleman, F.
Genomics 13, 257-263, 1992
A>Title: Platelet-derived growth factor A chain: confirmation of localization of PDGF
A:Reference number: A42002; MUID:92307656
A:Accession: B42002
A>Status: preliminary; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 152-196 <BO2>
R:Rorsman, F.; Bywater, M.; Knott, T.J.; Scott, J.; Betsholtz, C.
Mol. Cell. Biol. 8, 571-577, 1988
A>Title: Structural characterization of the human platelet-derived growth factor A-chain
A:Reference number: A28122; MUID:88174698
A:Accession: B28122
A:Molecule type: mRNA
A:Residues: 1-63, 'TRD', 67-196 <ROR>
A:CROSS-references: GB:M20488
A>Note: The authors translated the codon ACA for residue 64 as Arg, CGT for residue 6
C:Comment: Exon 6 is spliced out of this variant splice form. For the major splice fo
C:Keywords: alternative splicing; glycoprotein; growth factor; mitogen; platelet

Query Match 12.1% Score 89; DB 2; Length 196;
Best Local Similarity 26.8%; Pred. No. 0.1; Gaps 3;
Matches 22; Conservative 18; Mismatches 32; Indels 10;

QY 50 ANVVFPCLLIVQRGCGGTWNWRSCTCNSKTKVKKYHEVLQFPFGHIKRGRAKTM 109
| : | : | : | : | : | : | : | : | : | : | : | : |
Db 115 ANFLWPCEVEKRGTCGCC-----NTSSVKQPISRHHRSVKVAKE--YVRKKPKLKE- 166

QY 110 ALVDIQLDHHERCDCICSSRRP 131
| : | : | : | : | : | : | : | : | : | : | : | : |
Db 167 --VVRLLEHLECACATSLNP 186

RESULT 9
A48851 platelet-derived growth factor chain A precursor (version 2) - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 16-Jul-1999
C:Accession: A48851; I51891 R:Katayose, D.; Ohe, M.; Yamauchi, K.; Ogata, M.; Shirato, K.; Fujita, H.; Shibahara,
Am. J. Physiol. 264, L100-L106, 1993

A;Reference number: S61795; MUID:96178224
A;Accession: S61795
A;Status: nucleic acid sequence not shown; not compared with conceptual translation
A:Molecule type: mRNA
A;Residues: 70-419 <JOU1>
A;Note: this sequence has been revised in reference S69207
A;Accession: S71443
A:Molecule type: protein
A;Residues: 'X',104-120 <JOU2>
R;Lee, J.; Gray, A.; Yuan, J.; Luoh, S.M.; Avraham, H.; Wood, W.I.
submitted to the EMBL Data Library, December 1995
A;Description: Vascular endothelial growth factor related protein (VRP): A ligand and sp
A;Reference number: S69208
A;Accession: S69208
A:Molecule type: mRNA
A;Residues: 1-419 <LEE>
A;Cross-references: EMBL:U43142; NID:gl150988; PIDN:AAA85214.1; PID:gl150989
R;Morris, J.C.
submitted to the EMBL Data Library, May 1996
A;Reference number: H01557
A;Accession: G02659
A;Status: preliminary; translated from GB/EMBL/DDBY
A:Molecule type: mRNA
A;Residues: 1-419 <WOR>
A;Cross-references: EMBL:U58111; NID:gl373426; PIDN:AAB02909.1; PID:gl373427
C;Genetics:
A;Gene: GDB:VEGFC; VRP
A;Cross-references: GDB:3890883; OMIM:601528
F;1-12/Domain: signal sequence #status predicted <SIG>
F;13-102/Domain: propeptide #status predicted <PRO>
F;103-419/Product: vascular endothelial growth factor C #status experimental <MAT>

Query Match 12.6%; Score 93; DB 2; Length 419;
Best Local Similarity 20.7%; Pred.No. 0.085;
Matches 38; Conservative 20; Mismatches 50; Indels 76; Gaps 8;

QY : 22 LDRLNDAKRYSCPTPNYSVNIREELKANVVF--PRCLLVQRGGNGC----- 69
| ::::: | | | | | | | | | | | | | | |
Db 119 LKSIDNEWRKTQCPREVCIDVGKEFGVATNTFPKPCSVYRCGCCNSEGLQCMNTST 178

QY : 70 -----CGTVNRWRSCTNSGTIV-KKYHEVLQ----- 94
| | | | | | | | | | | | | | |
Db 179 SYLSKTLFEITVPLSQGPKPVTTISFANHTSCRCKSLDVYRVHSHIIRSLPATLPQQA 238

QY : 95 -----PEPGHKR-----RGRAKTMALVDI-----OLDHERDCICSS 128
| | | | | | | | | | | | | | |
Db 239 ANKTCPTNYMNNHICRLAQEDPFMFSDAGDDSTDGFHDICGNPKELD-EETCCVCRA 297

QY : 129 --RP 130
||
Db 298 GLRP 301

RESULT 7
A37359
platelet-derived growth factor chain A precursor - mouse
C:Species: Mus musculus (house mouse)
C>Date: 19-Mar-1993 #sequence_revision 19-Mar-1993 #text_change 07-May-1999
C;Accession: A37359
R;Mercola, M.; Wang, C.; Kelly, J.; Brownlee, C.; Jackson-Grusby, L.; Stiles, C.; Bowen
Dev. Biol. 138, 114-122, 1990
A;Title: Selective expression of PDGF A and its receptor during early mouse embryogenesis
A;Reference number: A37359; MUID:90169294
A;Accession: A37359
A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra
A:Molecule type: mRNA
A;Residues: 1-196 <MER>
A;Cross-references: GB:M29464
C;Superfamily: platelet-derived growth factor

Query Match 12.1%; Score 89; DB 2; Length 196;

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OM protein - protein search, using sw model

Run on: September 26, 2001, 15:15:09 ; Search time 12.26 Seconds
(without alignments)
221.691 Million cell updates/sec

Title: US-09-662-783-4
Perfect score: 737
Sequence: 1 MYLTPRYGRSHYDRKSKV.....DIQLDHHRCDCICSSRPPR 132

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 197339 seqs, 20590346 residues

Total number of hits satisfying chosen parameters: 197339

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents_AA:*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep.*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep.*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep.*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep.*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep.*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	103	14.0	321	4	US-08-915-795-9
2	103	14.0	325	4	US-08-915-795-3
3	103	14.0	354	4	US-08-915-795-5
4	103	14.0	358	4	US-08-915-795-8
5	95.5	13.0	102	1	US-08-469-427A-2
6	95.5	13.0	102	2	US-08-609-443B-2
7	95.5	13.0	102	2	US-08-569-063C-2
8	95.5	13.0	133	1	US-08-469-427A-9
9	95.5	13.0	133	2	US-08-609-443B-9
10	95.5	13.0	133	2	US-08-569-063C-9
11	95.5	13.0	188	1	US-08-469-427A-5
12	95.5	13.0	188	2	US-08-609-443B-5
13	95.5	13.0	188	2	US-08-569-063C-5
14	95.5	13.0	207	2	US-08-609-443B-13
15	95.5	13.0	207	2	US-08-569-063C-13
16	94	12.8	195	1	US-08-469-427A-7
17	94	12.8	195	2	US-08-609-443B-7
18	94	12.8	195	2	US-08-569-063C-7
19	93	12.6	350	2	US-08-999-811-4
20	93	12.6	350	2	US-08-824-996-2
21	93	12.6	350	3	US-09-042-105-4
22	93	12.6	350	4	US-08-510-133A-33
23	93	12.6	350	4	US-08-595-895-33
24	93	12.6	419	2	US-08-999-811-2
25	93	12.6	419	3	US-09-042-105-2
26	93	12.6	419	3	US-09-042-105-18
27	93	12.6	419	4	US-08-795-430-8

28	93	12.6	419	4	US-08-510-133A-35
29	93	12.6	419	5	PCT-US96-09001-2
30	92	12.5	415	4	US-08-795-430-11
31	89	12.1	104	6	5498600-4
32	89	12.1	110	1	US-08-095-898-2
33	89	12.1	110	2	US-08-804-953-1
34	89	12.1	110	5	PCT-US91-02766-14
35	89	12.1	110	5	PCT-US92-09439-2
36	89	12.1	125	1	US-07-883-949B-7
37	89	12.1	125	1	US-08-095-898-4
38	89	12.1	125	1	US-07-977-234C-7
39	89	12.1	125	5	PCT-US91-02766-16
40	89	12.1	125	5	PCT-US92-09439-4
41	89	12.1	126	6	5428135-4
42	89	12.1	196	1	US-08-469-427A-12
43	89	12.1	196	1	US-08-387-845-2
44	89	12.1	196	2	US-08-569-063C-22
45	89	12.1	196	2	US-08-999-811-5

ALIGNMENTS

RESULT 1
US-08-915-795-9
; Sequence 9, Application US/08915795
; Patent No. 6235713
; GENERAL INFORMATION:
; APPLICANT: Marc G. ACHEN
; APPLICANT: Andrew F. WILKS
; APPLICANT: Steven A. STACKER
; APPLICANT: Kari ALITALO
; TITLE OF INVENTION: GROWTH FACTOR
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Evenson, McKeown, Edwards & Lenahan P.L.L.C.
; STREET: 1200 G Street, NW, Suite 700
; CITY: Washington
; STATE: DC
; COUNTRY: United States of America
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/915,795
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: EVANS, Joseph D.
; REGISTRATION NUMBER: 26,269
; REFERENCE/DOCKET NUMBER: 1064/42983
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-8800
; TELEFAX: (202) 628-8844
; TELEX: N/A
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 321 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; TISSUE TYPE: Mouse Lung
US-08-915-795-9

Query Match 14.0%; Score 103; DB 4; Length 321;
Best Local Similarity 27.0%; Pred. No. 0.00039;
Matches 34; Conservative 17; Mismatches 47; Indels 28; Gaps 6;

Query Match 13.0%; Score 95.5; DB 1; Length 102;
Best Local Similarity 27.9%; Pred. No. 0.00068;
Matches 29; Conservative 16; Mismatches 38; Indels 21; Gaps 5;

Query Match	13.08;	Score	95.5;	DB	1;	Length	102;
Best Local Similarity	27.98;	Pred.	NO.	0.00068;			
Matches	29;	Conservative	16;	Mismatches	38;	Indels	21;
							Gaps
QY	31	RVSCTPRNYSNIREELKANV	--FPRCLLVORCGNGCGCTV	VNRSCTNSGKT	VKK	88	
DB	13	RATQCPREVVVPLSEL	-MGNVVQLVPSCVT	VRQCI	--GCCPDG	GLCEVPTG	QHV
QY	89	YHEVLQFEFGHKKRGRAKT	MALVDIQLDHHHERDCI	SSRRP	132		
DB	69	OTILMTOY	-----PSSOLGEMSL	EPHSOCEC	-----RP	KK	97

RESULT 6
US-08-609-443B-2
; Sequence 2, Application US/08609443B
; Patent No. 5840693
; GENERAL INFORMATION:
; APPLICANT: ERIKSSON, Ulf
; APPLICANT: OLOFSSON, Birgitta
; APPLICANT: ALITALO, Kari
; APPLICANT: PAJUSOLA, Katri
; TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR-B AND
; TITLE OF INVENTION: DNA CODING THEREFOR
; NUMBER OF SEQUENCES: 57
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Evenson, McKown, Edwards & Lenahan, P.L.L.C.
; STREET: 1200 G Street, N.W., Suite 700
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

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;
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/609,443B
; FILING DATE: 01-MAR-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/397,651
; FILING DATE: 01-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/469,427
; FILING DATE: 06-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/569,063
; FILING DATE: 06-DEC-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: EVANS, Joseph D
; REGISTRATION NUMBER: 26,269
; REFERENCE/DOCKET NUMBER: 1064/41979CP4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-8800
; TELEFAX: (202) 628-8844
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 102 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; TISSUE TYPE: mouse embryo
;
; US-08-609-443B-2
;
; Query Match 13.0%; Score 95.5; DB 2; Length 102;
; Best Local Similarity 27.9%; Pred. No. 0.00068;
; Matches 29; Conservative 16; Mismatches 38; Indels 21; Gaps 5;
;
; QY 31 RYSCPTPNYSVNIRELKLNVV--FPRLCLLVORCGGCGTGVNWRSCVTCNSGKTVKK 88
; Db 13 RATCQPREVVVPLSMEL-MGNVVKQLVPSCVTVORCG---GCCPDGDLCECVPTGQHQRVM 68
; QY 89 YHEVLOFEPGHKRRKRAKTMALVDIQLDHERCDICSSRRPPR 132
; Db 69 QILMIQY-----PSSQLGEMSLSEHSOCEC-----RPKK 97
;
; RESULT 7
; US-08-569-063C-2
; Sequence 2, Application US/08569063C
; Patent No. 5928939
; GENERAL INFORMATION:
; APPLICANT: ERIKSSON, Ulf
; APPLICANT: OLOFSSON, Birgitta
; APPLICANT: ALITALO, Kari
; APPLICANT: PAJUSOLA, Katri
; TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR-B AND
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Evenson, McKeown, Edwards & Lenahan, P.L.L.C.
; STREET: 1200 G Street, N.W., Suite 700
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
;
; US-08-569-063C-2
; Sequence 2, Application US/08569063C
; Patent No. 5928939
; GENERAL INFORMATION:
; APPLICANT: ERIKSSON, Ulf
; APPLICANT: OLOFSSON, Birgitta
; APPLICANT: ALITALO, Kari
; APPLICANT: PAJUSOLA, Katri
; TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR-B AND
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Evenson, McKeown, Edwards & Lenahan, P.L.L.C.
; STREET: 1200 G Street, N.W., Suite 700
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25

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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/569,063C
; FILING DATE: 06-DEC-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/469,427
; FILING DATE: 06-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/397,651
; FILING DATE: 01-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: EVANS, Joseph D
; REGISTRATION NUMBER: 26,269
; REFERENCE/DOCKET NUMBER: 1064/41979CP3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-8800
; TELEFAX: (202) 628-8844
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 102 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; TISSUE TYPE: mouse embryo
;
; US-08-569-063C-2
;
; Query Match 13.0%; Score 95.5; DB 2; Length 102;
; Best Local Similarity 27.9%; Pred. No. 0.00068;
; Matches 29; Conservative 16; Mismatches 38; Indels 21; Gaps 5;
;
; QY 31 RYSCPTPNYSVNIRELKLNVV--FPRLCLLVORCGGCGTGVNWRSCVTCNSGKTVKK 88
; Db 13 RATCQPREVVVPLSMEL-MGNVVKQLVPSCVTVORCG---GCCPDGDLCECVPTGQHQRVM 68
; QY 89 YHEVLOFEPGHKRRKRAKTMALVDIQLDHERCDICSSRRPPR 132
; Db 69 QILMIQY-----PSSQLGEMSLSEHSOCEC-----RPKK 97
;
; RESULT 8
; US-08-469-427A-9
; Sequence 9, Application US/08469427A
; Patent No. 5607918
; GENERAL INFORMATION:
; APPLICANT: Eriksson, Ulf
; APPLICANT: Olofsson, Birgitta
; APPLICANT: Alitalo, Kari
; APPLICANT: Pajusola, Katri
; TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR-B AND
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Evenson, McKeown, Edwards & Lenahan
; STREET: 1200 G Street, N.W., Suite 700
; CITY: Washington
; STATE: DC
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/469,427A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/397,651
; FILING DATE: 01-MAR-1995
; ATTORNEY/AGENT INFORMATION:

```

NAME: Evans, Joseph D
 REGISTRATION NUMBER: 26,269
 REFERENCE/DOCKET NUMBER: 41979cp2
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202) 628-8800
 TELEFAX: (202) 628-8844
 INFORMATION FOR SEQ ID NO: 9:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 133 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-469-427A-9

Query Match 13.0%; Score 95.5; DB 1; Length 133;
 Best Local Similarity 27.9%; Pred. No. 0.00095;
 Matches 29; Conservative 16; Mismatches 38; Indels 21; Gaps 5;
 QY 31 RYCTPRNYSVNIREEKLANV--FPRCLLVORCGGCGGTNNRSCCTCNSGKTVKK 88
 Db 44 RATQCPREVVPLSMEL-MGNVVKQLVPCVTVQRCG---GCCPDDGLECVPTGQHVRM 99
 QY 89 YHEVLOFEPGHIKRRGRAKTMALVDIQLDHHRCDCICSSRPPR 132
 Db 100 QILMIQY-----PSSQLGEMSLSEHSQCEC-----RPKK 128

RESULT 9
 US-08-609-443B-9
 Sequence 9, Application US/08609443B
 Patent No. 5840693
 GENERAL INFORMATION:
 APPLICANT: ERIKSSON, Ulf
 APPLICANT: OLOFSSON, Birgitta
 APPLICANT: ALITALO, Kari
 APPLICANT: PAJUSOLA, Katri
 TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR-B AND
 TITLE OF INVENTION: DNA CODING THEREFOR
 NUMBER OF SEQUENCES: 57
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Evenson, McKeown, Edwards & Lenahan, P.L.L.C.
 STREET: 1200 G Street, N.W., Suite 700
 CITY: Washington
 STATE: DC
 COUNTRY: USA
 ZIP: 20005

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/609,443B
 FILING DATE: 01-MAR-1996
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/397,651
 FILING DATE: 01-MAR-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/469,427
 FILING DATE: 06-JUN-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/569,063
 FILING DATE: 06-DEC-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: EVANS, Joseph D
 REGISTRATION NUMBER: 26,269
 REFERENCE/DOCKET NUMBER: 1064/41979CP4
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202) 628-8800
 TELEFAX: (202) 628-8844

INFORMATION FOR SEQ ID NO: 9:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 133 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-609-443B-9

Query Match 13.0%; Score 95.5; DB 2; Length 133;
 Best Local Similarity 27.9%; Pred. No. 0.00095;
 Matches 29; Conservative 16; Mismatches 38; Indels 21; Gaps 5;
 QY 31 RYCTPRNYSVNIREEKLANV--FPRCLLVORCGGCGGTNNRSCCTCNSGKTVKK 88
 Db 44 RATQCPREVVPLSMEL-MGNVVKQLVPCVTVQRCG---GCCPDDGLECVPTGQHVRM 99
 QY 89 YHEVLOFEPGHIKRRGRAKTMALVDIQLDHHRCDCICSSRPPR 132
 Db 100 QILMIQY-----PSSQLGEMSLSEHSQCEC-----RPKK 128

RESULT 10
 US-08-569-063C-9
 Sequence 9, Application US/08569063C
 Patent No. 5928939
 GENERAL INFORMATION:
 APPLICANT: ERIKSSON, Ulf
 APPLICANT: OLOFSSON, Birgitta
 APPLICANT: ALITALO, Kari
 APPLICANT: PAJUSOLA, Katri
 TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR-B AND
 TITLE OF INVENTION: DNA CODING THEREFOR
 NUMBER OF SEQUENCES: 23
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Evenson, McKeown, Edwards & Lenahan, P.L.L.C.
 STREET: 1200 G Street, N.W., Suite 700
 CITY: Washington
 STATE: DC
 COUNTRY: USA
 ZIP: 20005

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/569,063C
 FILING DATE: 06-DEC-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/469,427
 FILING DATE: 06-JUN-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/397,651
 FILING DATE: 01-MAR-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: EVANS, Joseph D
 REGISTRATION NUMBER: 26,269
 REFERENCE/DOCKET NUMBER: 1064/41979CP3
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202) 628-8800
 TELEFAX: (202) 628-8844
 INFORMATION FOR SEQ ID NO: 9:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 133 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-569-063C-9

Db 100 QILMIQY-----PSSQLGEMSLSEHSQCCEC-----RPKK 128

RESULT 12
US-08-609-443B-5
; Sequence 5, Application US/08609443B
; Patent No. 5840693
; GENERAL INFORMATION:
; APPLICANT: ERIKSSON, Ulf
; APPLICANT: OLOFSSON, Birgitta
; APPLICANT: ALITALO, Kari
; APPLICANT: PAJUSOLA, Katri
; TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR-B AND
; TITLE OF INVENTION: DNA CODING THEREFOR
; NUMBER OF SEQUENCES: 57
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Evenson, McKeown, Edwards & Lenahan, P.L.L.C.
; STREET: 1200 G Street, N.W., Suite 700
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/609,443B
; FILING DATE: 01-MAR-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/397,651
; FILING DATE: 01-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/469,427
; FILING DATE: 06-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/569,063
; FILING DATE: 06-DEC-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: EVANS, Joseph D
; REGISTRATION NUMBER: 26,269
; REFERENCE/DOCKET NUMBER: 1064/41979CP4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-8800
; TELEFAX: (202) 628-8844
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 188 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; TISSUE TYPE: adult mouse heart
; US-08-609-443B-5

Query Match 13.08; Score 95.5; DB 2; Length 188;
Best Local Similarity 27.99; Pred. No. 0.0015;
Matches 29; Conservative 16; Mismatches 38; Indels 21; Gaps 5;

QY 31 RYSCTPRNYSYNIREELKANLV--FFPRCLLLVQRGGNCGGTVMNRSCITCSNGSKTVKK 88
| | | | | : | | | | | : | | | | | : |
| | | | | : | | | | | : | | | | | : |

Db 44 RATCQPREVVVPLSMEL-MGNVVKLVPSCVTVQRCG---GCCPDGLCECVTGQHVRM 99
| | | | | : | | | | | : | | | | | : |

QY 89 YHEVLQEPGHIKRRGRAKTWALVDIQLDHHERCDCICSSRPPR 132
::: : | : | : | : | : | : | : |

Db 100 QILMIQY-----PSSQLGEMSLSEHSQCCEC-----RPKK 128

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RESULT 13
US-08-569-063C-5
; Sequence 5, Application US/08569063C
; Patent No. 5928939
; GENERAL INFORMATION:
; APPLICANT: ERIKSSON, Ulf
; APPLICANT: OLOFSSON, Birgitta
; APPLICANT: ALITALO, Kari
; APPLICANT: PAJUSOLA, Katri
; TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR-B AND
; TITLE OF INVENTION: DNA CODING THEREFOR
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Evenson, McKeown, Edwards & Lenahan, P.L.L.C.
; STREET: 1200 G Street, N.W., Suite 700
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/569,063C
; FILING DATE: 06-DEC-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/469,427
; FILING DATE: 06-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/397,651
; FILING DATE: 01-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: EVANS, Joseph D
; REGISTRATION NUMBER: 26,269
; REFERENCE/DOCKET NUMBER: 1064/41979CP3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-8800
; TELEFAX: (202) 628-8844
; INFORMATION FOR SEQ ID NO: 5:
; LENGTH: 188 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; TISSUE TYPE: adult mouse heart
; US-08-569-063C-5

Query Match 13.0%; Score 95.5; DB 2; Length 188;
Best Local Similarity 27.9%; Pred. No. 0.0015;
Matches 29; Conservative 16; Mismatches 38; Indels 21; Gaps 5;

QY 31 RYSCPTPRNYSVNIRELKLANVV--FFPCLLVQRCGCGTNNWRSCTCNSGKTVKK 88
Db 44 RATCPQREVVPVPLSMEL-MGNVVKQLVPSCVTVQRCG---GCCPDDGLECVPTGQHVRM 99

QY 89 YHEVLQFEPGHKRRGAKTMAVDIQLDHERCDDICSSRPPR 132
Db 100 QILMIQY-----PSSQLGEMSLSEHSQCEC-----RPKK 128

RESULT 14
US-08-609-443B-13
; Sequence 13, Application US/08609443B
; Patent No. 5840693
; GENERAL INFORMATION:
; APPLICANT: ERIKSSON, Ulf
; APPLICANT: OLOFSSON, Birgitta

```

```

; APPLICANT: ALITALO, Kari
; APPLICANT: PAJUSOLA, Katri
; TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR-B AND
; TITLE OF INVENTION: DNA CODING THEREFOR
; NUMBER OF SEQUENCES: 57
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Evenson, McKeown, Edwards & Lenahan, P.L.L.C.
; STREET: 1200 G Street, N.W., Suite 700
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/609,443B
; FILING DATE: 01-MAR-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/397,651
; FILING DATE: 01-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/469,427
; FILING DATE: 06-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/569,063
; FILING DATE: 06-DEC-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: EVANS, Joseph D
; REGISTRATION NUMBER: 26,269
; REFERENCE/DOCKET NUMBER: 1064/41979CP4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-8800
; TELEFAX: (202) 628-8844
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 207 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; TISSUE TYPE: mouse
; US-08-609-443B-13

Query Match 13.0%; Score 95.5; DB 2; Length 207;
Best Local Similarity 27.9%; Pred. No. 0.0017;
Matches 29; Conservative 16; Mismatches 38; Indels 21; Gaps 5;

QY 31 RYSCPTPRNYSVNIRELKLANVV--FFPCLLVQRCGCGTNNWRSCTCNSGKTVKK 88
Db 44 RATCPQREVVPVPLSMEL-MGNVVKQLVPSCVTVQRCG---GCCPDDGLECVPTGQHVRM 99

QY 89 YHEVLQFEPGHKRRGAKTMAVDIQLDHERCDDICSSRPPR 132
Db 100 QILMIQY-----PSSQLGEMSLSEHSQCEC-----RPKK 128

RESULT 15
US-08-569-063C-13
; Sequence 13, Application US/08569063C
; Patent No. 5928939
; GENERAL INFORMATION:
; APPLICANT: ERIKSSON, Ulf
; APPLICANT: OLOFSSON, Birgitta
; APPLICANT: ALITALO, Kari
; APPLICANT: PAJUSOLA, Katri
; TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR-B AND
; TITLE OF INVENTION: DNA CODING THEREFOR
; NUMBER OF SEQUENCES: 23

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Search completed: September 26, 2001, 15:16:18
Job time: 69 sec

OM of: US-09-662-783-4 to: GenEmbl.* out_format : pfs

Date: Sep 26, 2001 8:53 PM

About: Results were produced by the GenCore software, version 4.5,
Copyright (c) 1993-2000 Compugen Ltd.

Command line parameters:

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Search information block:

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Database sequences: 1344157
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gb_prl:AY027517	+	737.00	1399.41	1.0e-69	3729	AY027517 Homo sapiens iris-exf
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DEFINITION complete cds.
ACCESSION AB033832
VERSION AB033832.1 GI:11602807
KEYWORDS spinal cord-derived growth factor-B; SCDGF-B.
SOURCE Homo sapiens Glioma cell_line:U373MG CDNA to mRNA.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (sites)
AUTHORS Hamada,T., Ui-Tei,K., Imaki,J. and Miyata,Y.
TITLE Molecular Cloning of SCDGF-B, a Novel Growth Factor Homologous to
SCDGF/PDGF-C/fallotet
JOURNAL Biochem. Biophys. Res. Commun. 280 (3), 733-737 (2001)
PUBMED 11162582
REFERENCE 2 (bases 1 to 1428)
AUTHORS Hamada,T., Ui-Tei,K. and Miyata,Y.
TITLE Direct Submission
JOURNAL Submitted (25-OCT-1999) Tsuyoshi Hamada, Nippon Medical School,
Department of Pharmacology; 1-1-5, Sendagi, Bunkyo-ku, Tokyo
113-8602, Japan (E-mail:t-hamada@nms.ac.jp,
Tel:81-3-3822-2131(ex.5277), Fax:81-3-5814-1684)
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DEFINITION Homo sapiens Iris-expressed growth factor short form (IEGF) mRNA,
complete cds, alternatively spliced.
ACCESSION  AY027518
VERSION     AY027518.1 GI:13432062
KEYWORDS   .
SOURCE     human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 3710)
            Wistow,G.
            Iris-expressed Growth Factor (IEGF)
            Unpublished
            JOURNAL
REFERENCE  2 (bases 1 to 3710)
            Wistow,G.
            Direct Submission
            Submitted (13-FEB-2001) MSF, NEI, 6/331, NIH, Bethesda, MD
            JOURNAL
            20892-2740, USA
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gene
CDS

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US-09-662-783-4 x AY027518 ..

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DEFINITION Homo sapiens iris-expressed growth factor long form (IEGF) mRNA,
complete cds, alternatively spliced.

ACCESSION AY027517

VERSION AY027517.1 GI:13432060

KEYWORDS

SOURCE human.

ORGANISM

Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

Wistow,G.
Iris-expressed Growth Factor (IEGF)

AUTHORS

Unpublished

JOURNAL

REFERENCE 2 (bases 1 to 3729)

AUTHORS

Wistow,G.
Direct Submission

TITLE

Submitted (13-FEB-2001) MSF, NEI, 6/331, NIH, Bethesda, MD

JOURNAL

20892-2740, USA
Location/Qualifiers

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DEFINITION Homo sapiens MSTP036 mRNA, complete cds.

3739 bp mRNA

PRI

12-DEC-2000

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ACCESSION AF113216
VERSION AF113216.1 GI:11640579
KEYWORDS
SOURCE human
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 3739)
AUTHORS Liu, B., Liu, Y.Q., Wang, X.Y., Zhao, B., Sheng, H., Zhao, X.W., Liu, S.,
Xu, Y.Y., Ye, J., Song, L., Gao, Y., Zhang, C.L., Zhang, J., Wei, Y.J.,
Cao, H.Q., Zhao, Y., Liu, L.S., Ding, J.F., Gao, R.L., Wu, Q.Y.,
Qiang, B.Q., Yuan, J.G., Liew, C.C., Zhao, M.S. and Hui, R.T.
TITLE Direct Submission
JOURNAL Submitted (15-DEC-1998) Molecular Medical Center for Cardiovascular
Disease, Cardiovascular Institute, CAMS & PUMC, 167, Bei Li Shi Lu,
Beijing 100037, P.R. China
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ACCESSION AX044538
VERSION AX044538.1 GI:11343390
KEYWORDS house mouse.
SOURCE Mus musculus
ORGANISM Mus musculus
REFERENCE 1 (bases 1 to 1472)
AUTHORS Gilbert, T., Hart, C.E., Sheppard, P.O. and Gilbertson, D.G.
TITLE Growth factor homolog zvegfa
JOURNAL Patent: WO 0066736-A, 52 09-NOV-2000;
Zymogenetics, Inc. (US)
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PGFKIYSEVEDFQAASETNNWSTSSISGVNSPSTPTLIADALDKKIAEFD
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HSVNLREEKLNAVYFFPRCLLVQRCGNGCGGTWNWKSCTCSGKTVKKYHEVLKFE
PGHKRRGRKAKNMALVDIQLDHHERCDCICSSRPPR"
BASE COUNT 434 a 327 c 332 g 379 t
ORIGIN

alignment_scores:
Quality: 686.00 Length: 132
Ratio: 5.197 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 90.152

alignment_block:
US-09-662-783-4 x AX044538 ..
Align seg 1/1 to: AX044538 from: 1 to: 1472
1 MetTyrLeuAspThrProArgTyrArgGlyArgSerTyrHisAspArgLy 17
807 TTGTATCTGGACACCCCTCATATTAGAGCGAGGTACATACCATGATCGAA 856
17 sSerLysValAspLeuAspArgLeuAsnAspAspAlaLysArgTyrSerC 34
857 GTCAAAAGTTGACCTGGACAGGCTCAATGATGATGATCAAGCGTTACAGTT 906
34 ysThrProArgAsnTyrSerValAsnIleArgGluGluLeuLysLeuAla 50
907 GCACCTCCAGGAATCACTCTGTGAACCTCAGGAGGAGCTGAAGCTGACC 956
51 AsnValValPhePheProArgCysLeuLeuValGlnArgCysGlyGlyAs 67
957 AATGCACTCTTCTTCCACGATGCTCCTCGTCGAGCGCTGTGGTGGCAA 1006
67 nCysGlyCysGlyThrValAsnTrpArgSerCysThrCysAsnSerGlyL 84
1007 CTGTGGTGTGGGAACTGTCAACTGGAAGTCTCGACATGCACTGACGTACGGA 1056
|||||
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84 ysthrValLysLysTyrHisGluValLeuGluInPheGluProGlyHisIle 100
 |||||
 1057 AGACAGTGAAGAAGTATCATGAGGTATTGAAGTTTGAGCCTGGACATTTC 1106
 |||||
 101 LysArgArgGlyArgAlaLysThrMetAlaLeuValAspIleGlnLeuAs 117
 |||||
 1107 AAGAGAAGGGGCAAGCTAAGAATATGGCTCTTGTGTATCCAGCTGGA 1156
 |||||
 117 phisHisGluArgCysAspCysIleCysSerSerArgProProArg 132
 |||||
 1157 TCATCATGAGCGATGCTGCTATCTGCTGAGCTCAAGACCACTCGA 1202
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seq_name: gb_fol:AB052170

seq_documentation_block:

LOCUS AB052170 1386 bp mRNA ROD 10-FEB-2001
 DEFINITION Rattus norvegicus rSCDGF-B mRNA for spinal-cord derived growth factor-B, complete cds.

ACCESSION AB052170

VERSION AB052170.1 GI:11610600

KEYWORDS Rattus norvegicus cdna to mRNA.

SOURCE Rattus norvegicus

ORGANISM Rattus norvegicus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Rattus.

REFERENCE 1 (sites)

Hamada,T., Ui-Tei,K., Imaki,J. and Miyata,Y.

Molecular Cloning of SCDGF-B, a Novel Growth Factor Homologous to

SCDGF/PDGF-C/fallotelin

Biochem. Biophys. Res. Commun. 280 (3), 733-737 (2001)

REFERENCE 2 (bases 1 to 1386)

Hamada,T., Ui-Tei,K. and Miyata,Y.

Direct Submission

Submitted (05-DEC-2000) Tsuyoshi Hamada, Nippon Medical School,

Department of Pharmacology; Sendagi 1-1-5, Bunkyo, Tokyo 113-8602,

Japan (E-mail:t-hamada@nms.ac.jp, Tel:81-3-3822-2131(ex.5277),

Fax:81-3-5814-1684)

FEATURES

Location/Qualifiers

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/organism="Rattus norvegicus"

/db_xref="taxon:10116"

160..1272

/gene="rSCDGF-B"

160..1272

/gene="rSCDGF-B"

/codon_start=1

/product="spinal-cord derived growth factor-B"

/protein_id="BAB18920.1"

/db_xref="GI:11610601"

/translation="MPELILVSTILVCANFCYRDTFATPOSASIKALRNANLRDSEN
 HLDDLYRRDENIRVTGCHVQSPFPNSYPRNLLLWRLSQEKTRIQLFADHQFGL
 EAENDICRDEVEDVESSTVVRGRCGHKEIPPRITRTNQIKITFOSDDYFVAK
 PGKIYFYFDEPEAAEINWESVTSFSGVSHSPSYMDSLTADALDKAIEFD
 TVEDLLKYFNPASQDLENDYMDTPYRGSRYSHERKSKVDLRLNDVKKRYCTPRN
 HSNVRLRELKLTNAVFPCLLVQRCGNGCGCTLNWKSCTCSSGKTVKKYHEVLKFE
 PGPKRGKAKNALVDIQLDHERCDICSSRPPR"

BASE COUNT 383 a 330 c 332 g 341 t

ORIGIN

alignment_scores:

Quality: 682.00 Length: 132

Ratio: 5.167 Gaps: 0

Percent Similarity: 100.000 Percent Identity: 88.636

alignment_block:

US-09-662-783-4 x AB052170 ..

Align seg 1/1 to: AB052170 from: 1 to: 1386

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|||||
 874 TTGTACATGGACACCCCTCGTTATAGGCGAGGTTCATACCATGAACGAA 923
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 17 sSerLysValAspLeuAspArgLeuAsnAspAlaLysArgTyrSerC 34
 |||||
 924 GTCTAAAGTGGACCTGGAGAGGCTCAATGATGATGCTCAAGCGTTACAGTT 973
 |||||
 34 ysthrProArgAsnTyrSerValAsnIleArgGluGluLeuLysLeuAla 50
 |||||
 974 GCACCTCCAGGAATACACTCGGTGATCTCAGGGAGGAGTTGAAGCTGACC 1023
 |||||
 51 AsnValValPhePheProArgCysLeuValGlnArgCysGlyGlyAs 67
 |||||
 1024 AACGCAGTCTTCTTCCACGATGCTCTTGTGCACGCTGTGTGGCAA 1073
 |||||
 67 nCysGlyCysGlyThrValAsnTrpArgSerCysThrCysAsnSerGlyL 84
 |||||
 1074 CTGTGGTTCGCGAACTCTCAACTGGAAGTCTTCGATATCCAGTTGGA 1123
 |||||
 84 ysthrValLysLysTyrHisGluValLeuGluInPheGluProGlyHisIle 100
 |||||
 1124 AGACAGTAAAGAAGTATCATGAGGTACTGAAGTTTGAGCCTGGACATTTC 1173
 |||||
 101 LysArgArgGlyArgAlaLysThrMetAlaLeuValAspIleGlnLeuAs 117
 |||||
 1174 AAAGAAGGGGCAAGCTAAGAATATGGCTCTTGTGATATCCAGTTGGA 1223
 |||||
 117 phisHisGluArgCysAspCysIleCysSerSerArgProProArg 132
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 1224 TCATCATGAGCGATGCTGCTATCTGCTGAGCTCAAGACCACTCGA 1269
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seq_name: gb_pat1:AX044492

seq_documentation_block:

LOCUS AX044492 1110 bp DNA PAT 24-NOV-2000

DEFINITION Sequence 6 from Patent WO00066736.

ACCESSION AX044492

VERSION AX044492.1 GI:11343347

KEYWORDS

SOURCE synthetic construct.

ORGANISM synthetic construct

REFERENCE 1 (bases 1 to 1110)

AUTHORS Gilbert,T., Hart,C.E., Sheppard,P.O. and Gilbertson,D.G.

TITLE Growth factor homolog zveg4

JOURNAL Patent: WO 0066736-A 6-09-NOV-2000;

ZymoGenetics, Inc. (US)

FEATURES

Location/Qualifiers

source

1..1110

/organism="synthetic construct"

/db_xref="taxon:32630"

/notes="degenerate sequence"

BASE COUNT 215 a 94 c 178 g 139 t 484 others

ORIGIN

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Quality: 554.00 Length: 131

Ratio: 5.276 Gaps: 0

Percent Similarity: 80.153 Percent Identity: 74.046

alignment_block:

US-09-662-783-4 x AX044492 ..

Align seg 1/1 to: AX044492 from: 1 to: 1110

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715 ATGTAYTYNGAYACCCNMGNTAYMGNGMGNWSNTAYCAYGAYMGNA 764

|||||

17 sSerLysValAspLeuAspArgLeuAsnAspAlaLysArgTyrSerC 34

|||||

765 RWSNAARGTNGAYTYNGAYMGNTNAAAYGAYGAYGCNAARMGNTAYSNT 814

|||||

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34 ysthrProArgAsnTyrSerValasnlleArgGluGluLeuLysLeuAla 50
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815 GYACNCCMGNAAYTAYWSNGTNAAYATHMGNGARGARYTNAARYTNGCN 864

51 AsnValValPheProArgCysLeuValGlnArgCysGlyGlyAs 67
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
865 AAYGTGNTNTTYYTCNMGNTGYTNTYNTGTCNARMGNTCYGGNGNAA 914

67 nCysGlyCysGlyThrValAsnTyrArgSerCysThrCysAsnSerGlyL 84
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
915 YTGCGGTGGNACNCTNAAYTCGMNWSNTGYACNTGAAAYWSNGNA 964

84 ysthrValLysLysTyrHisGluValLeuGlnPheGluProGlyHisIle 100
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
965 ARACNGTNAARARTAYCAYGARGTNTNCARTTYGARCNGGNCAYATH 1014

101 LysArgArgGlyArgAlaLysThrMetAlaLeuValAspIleGlnLeuAs 117
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1015 AARMGNGNGNGMGNGCNAARACNATGCGNYTNGTNGAYATHCARTNGA 1064

117 pHisHisGluArgCysAspCysIleCysSerArgProPro 131
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
1065 YCAYCARGMGNTGYGAYTGATHTGTWSNMGMCNCCN 1107

seq_name: gb_htg14:AC067870

seq_documentation_block:
LOCUS AC067870 160345 bp DNA HTG 23-JUN-2000
DEFINITION Homo sapiens chromosome 11 clone RP11-475J2 map 11, WORKING DRAFT
SEQUENCE, 18 unordered pieces.
ACCESSION AC067870
VERSION AC067870.3 GI:8671974
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 160345)
Birken.B., Linton.L., Nusbaum.C., Lander.E., Abraham.H., Allen.N.,
Anderson.S., Balgwin.J., Barna.N., Bastien.V., Beda.F.,
Boguslavsky.L., Boukhgalter.B., Brown.A., Burkett.G.,
Campopiano.A., Castile.A., Choepel.Y., Colangelo.M., Collins.S.,
Collamore.A., Cooke.P., Dearellano.K., Dewar.K., Diaz.J.S.,
Dodge.S., Domino.M., Doyle.M., Ferreira.P., FitzHugh.W., Gage.D.,
Galagan.J., Gardyna.S., Ginde.S., Goyette.M., Graham.L.,
Grand-Pierre.N., Grant.G., Hagos.B., Heaford.A., Horton.L.,
Howland.J.C., Iliev.I., Johnson.R., Jones.C., Kann.L., Karatas.A.,
Klein.J., Larocque.K., Lamazares.R., Landers.T., Lehoczkv.J.,
Levine.R., Lieu.C., Liu.G., Locke.K., Macdonald.P., Marquis.N.,
McCarthy.M., McEwan.P., McGurk.A., McKernan.K., McPheeters.R.,
Meldrum.J., Meneus.L., Mihova.T., Miranda.C., Mlenga.V., Morrow.J.,
Murphy.T., Naylor.J., Norman.C.H., O'Connor.K., O'Donnell.P.,
O'Neil.D., Oliver.T.M., Oliver.J., Peterson.K., Pierre.N.,
Pisani.C., Pollara.V., Raymond.C., Riley.R., Rogov.P., Rothman.D.,
Roy.A., Santos.R., Schauer.S., Severi.P., Spencer.B.,
Stange-Thomann.N., Stojanovic.N., Subramanian.A., Talamas.J.,
Tessaye.S., Theodore.J., Tirrell.A., Travers.M., Trigilio.J.,
Vassiliev.H., Viel.R., Vo.A., Wilson.B., Wu.X., Wyman.D., Ye.W.J.,
Young.G., Zainoun.J., Zimmer.A. and Zody.M.
Direct Submission
Submitted (27-APR-2000) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Jun 23, 2000 this sequence version replaced gi:8099852.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
FEATURES
source
1..160345
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="11"
/map="11"
/clone="RP11-475J2"
/clone_lib="RPC1-11 Human Male BAC"
1..946
/note="assembly_fragment
clone_end:77
vector_side:right"
misc_feature
1..946
/note="assembly_fragment
clone_end:77
vector_side:right"

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Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: L8810
Center clone name: 475_J2
----- Summary Statistics
Sequencing vector: M13; M77815; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 151812 bases at least Q40
Consensus quality: 156075 bases at least Q30
Consensus quality: 157717 bases at least Q20
Insert size: 163000; agarose-fp
Quality coverage: 4.9 in Q20 bases; agarose-fp
Quality coverage: 5.0 in Q20 bases; sum-of-contigs
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* NOTE: This is a 'working draft' sequence. It currently
* consists of 18 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
*
* 1 946: contig of 946 bp in length
* 947 1046: gap of 100 bp
* 1047 2803: contig of 1757 bp in length
* 2804 2903: gap of 100 bp
* 2904 4474: contig of 1571 bp in length
* 4475 4574: gap of 100 bp
* 4575 8112: contig of 3538 bp in length
* 8113 8212: gap of 100 bp
* 8213 11442: contig of 3230 bp in length
* 11443 11542: gap of 100 bp
* 11543 14027: contig of 2485 bp in length
* 14028 14127: gap of 100 bp
* 14128 17482: contig of 3355 bp in length
* 17483 17582: gap of 100 bp
* 17583 20007: contig of 2425 bp in length
* 20008 20107: gap of 100 bp
* 20108 26548: contig of 6441 bp in length
* 26549 34423: contig of 7775 bp in length
* 34424 34523: gap of 100 bp
* 34524 41559: contig of 7036 bp in length
* 41560 41659: gap of 100 bp
* 41660 50886: contig of 9227 bp in length
* 50887 50986: gap of 100 bp
* 50987 64203: contig of 13217 bp in length
* 64204 64303: gap of 100 bp
* 64304 75627: contig of 11324 bp in length
* 75628 75727: gap of 100 bp
* 75728 91802: contig of 16075 bp in length
* 91803 91902: gap of 100 bp
* 91903 110040: contig of 18138 bp in length
* 110041 110140: gap of 100 bp
* 110141 130770: contig of 20630 bp in length
* 130771 130870: gap of 100 bp
* 130871 160345: contig of 29475 bp in length.
Location/Qualifiers
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="11"
/map="11"
/clone="RP11-475J2"
/clone_lib="RPC1-11 Human Male BAC"
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/note="assembly_fragment
clone_end:77
vector_side:right"
misc_feature
1..946
/note="assembly_fragment
clone_end:77
vector_side:right"

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misc_feature 1047..2803
/contig="assembly_fragment"
misc_feature 2904..4474
/contig="assembly_fragment"
misc_feature 4575..8112
/contig="assembly_fragment"
misc_feature 8213..11442
/contig="assembly_fragment"
misc_feature 11543..14027
/contig="assembly_fragment"
misc_feature 14128..17482
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misc_feature 17583..20007
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/contig="assembly_fragment"
vector_side:right"
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misc_feature 26649..34423
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misc_feature 64304..75627
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misc_feature 110141..130770
/contig="assembly_fragment"
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/contig="assembly_fragment"
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ORIGIN

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  Ratio: 5.603        Gaps: 0
  Percent Similarity: 100.000  Percent Identity: 100.000

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US-09-662-783-4 x AC067870/rev ..

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18997 GTTGACCTGGATAGGCTCAATGATGATGCGACAGCTTACAGTTGCACTCC 18948
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36 oArgAsnTyrSerValAsnIleArgGluGluLeuLysLeuAlaAsnValV 53
|||||
18947 CAGGAATTACTCGTCAATATAAGAGAAGAGCTGAAGTTGGCAATGTGG 18898
|||||

53 alPhePheProArgCysLeuLeuValGlnArgCysGlyLysCysGly 69
18897 TCTTCTTTCCAGCTTCCCTCCCTCGTGCAGCGCTGTGAGGAAATTTGGC 18848
|||||

70 CysGlyThrValAsnTrpArgSerCysThrCysAsnSerGlyLysThrVa 86
|||||
18847 TGTGGAACTGTCACTGGAGGCTCTGCACATGCAATTCAGGGAACCGT 18798
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86 llLysLysTyrHisGluVal 92
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18797 GAAAGAGTATCATGAGGTA 18779

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seq_documentation_block:

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LOCUS      AP002989 164771 bp DNA HTG 05-DEC-2000
DEFINITION Homo sapiens chromosome 11 clone RP11-475J2 map 11q, WORKING DRAFT
SEQUENCE, 14 unordered pieces.
ACCESSION  AP002989
VERSION     AP002989.1 GI:11559304
KEYWORDS   HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE      Homo sapiens DNA, clone:RP11-475J2.
ORGANISM    Homo sapiens
            Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 164771)
AUTHORS     Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
            Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
TITLE       Homo sapiens 164,771 genomic DNA of 11q
JOURNAL     Published Only in DataBase (2000) In press
REFERENCE   2 (bases 1 to 164771)
AUTHORS     Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
            Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
TITLE       Direct Submission
JOURNAL     Submitted (01-DEC-2000) Masahira Hattori, The Institute of Physical
            and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
            1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
            (E-mail:hattori@gsr.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
            tel:81-45-503-9111, fax:81-45-503-9170)
COMMENT     ----- Genome Center
            Center: RIKEN Genomic Sciences Center(GSC)
            Center code: RIKEN
            Web site: http://hgp.gsc.riken.go.jp/
            Contact: hattori@gsr.riken.go.jp
            ----- Project Information
            Center project name: HumDraft11
            Center clone name: RP11-475J2
            ----- Summary Statistics
            Sequencing vector: PCR products; 100% of reads
            Chemistry: Dye-terminator ET-amersham; 100% of reads
            Assembly program: Phrap; version 0.990329
            Consensus quality: 161781 bases at least Q40
            Consensus quality: 162965 bases at least Q30
            Consensus quality: 163349 bases at least Q20
            Insert size: 163471; sum-of-contigs
            Quality coverage: 8.50x in Q20 bases; sum-of-contigs
            -----
NOTE: This is a 'working draft' sequence. It currently consists of
14 contigs. The true order of the pieces is not known and their
order in this sequence record is arbitrary. Gaps between the
contigs are represented as runs N, but the exact sizes of the gaps
are unknown. This record will be updated with the finished sequence
as soon as it is available and the accession number will be
preserved
1 34180 contig of 34180 bp in length
34281 68840 contig of 34560 bp in length
68941 90300 contig of 21360 bp in length
90401 106732 contig of 16332 bp in length
106833 119529 contig of 12697 bp in length
119630 131965 contig of 12336 bp in length
132066 139832 contig of 7767 bp in length
139933 146362 contig of 6430 bp in length
146463 148684 contig of 2222 bp in length
148785 153951 contig of 5167 bp in length
154052 158926 contig of 4875 bp in length
159027 161395 contig of 2369 bp in length
161496 163230 contig of 1735 bp in length
163331 164771 contig of 1441 bp in length.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 14 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
1 34180: contig of 34180 bp in length
* 34181 34280: gap of 100 bp

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* 34281 68840: contig of 34560 bp in length
* 68841 68940: gap of 100 bp
* 68941 90300: contig of 21360 bp in length
* 90301 90400: gap of 100 bp
* 90401 106732: contig of 16332 bp in length
* 106733 106832: gap of 100 bp
* 106833 119529: contig of 12697 bp in length
* 119530 119629: gap of 100 bp
* 119630 131965: contig of 12336 bp in length
* 131966 132065: gap of 100 bp
* 132066 132065: gap of 100 bp
* 132066 139832: contig of 7787 bp in length
* 139833 139932: gap of 100 bp
* 139933 146362: contig of 6430 bp in length
* 146363 146462: gap of 100 bp
* 146463 148684: contig of 2222 bp in length
* 148685 148784: gap of 100 bp
* 148785 153951: contig of 5167 bp in length
* 153952 154051: gap of 100 bp
* 154052 158926: contig of 4875 bp in length
* 158927 159026: gap of 100 bp
* 159027 161395: contig of 2369 bp in length
* 161396 161495: gap of 100 bp
* 161496 163230: contig of 1735 bp in length
* 163231 163330: gap of 100 bp
* 163331 164771: contig of 1441 bp in length.

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FEATURES

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/db_xref="taxon:9606"
/chromosome="11"
/map="11q"
/clone="RP11-475J2"

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misc_feature

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106833..119529
/note="assembly_fragment"
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146463..148684
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148785..153951
/note="assembly_fragment"
154052..158926
/note="assembly_fragment"
159027..161395
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BASE COUNT 51433 a 31186 c 32085 g 48767 t 1300 others
ORIGIN

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alignment_scores:

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Quality: 409.00 Length: 73
Ratio: 5.603 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

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alignment_block:

US-09-662-783-4 x AP002989/rev ..

Align seg 1/1 to reverse of: AP002989 from: 1 to: 164771

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160385 GTTGACCTGGATAGCGTCATGATGCGCAAGCGTTACAGTTGCACTCC 160336

36 oArgAsnTyrSerValAsnIleArgGluLeuLeuLysLeuAlaAsnValV 53
|||||
160335 CAGGAATTACTCGGTCAATATAAGAGAAGAGCTGAAGTTGGCAATGTGG 160286

53 alpHePheProArgCysLeuLeuValGlnArgCysGlyGlyAsnCysGly 69
|||||
160285 TCCTCTTTCCACGTTGCTCTCTGTCAGCGCTGTGGAGGAATGTGGC 160236

70 CysGlyThrValAsnTrpArgSerCysThrCysAsnSerGlyLysThrVa 86
|||||
160235 TGTGGAACCTGTCACTGGAGGTCTGCACATGCAATTCAGGGAAACCGT 160186

86 lLysLysTyrHisGluVal 92
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160185 GAAAAGTATCATGAGGTA 160167

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seq_name: gb_htg24:AP003043

seq_documentation_block:

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LOCUS AP003043 180709 bp DNA HTG 14-DEC-2000
DEFINITION Homo sapiens chromosome 11 clone RP11-617B3 map 11q, WORKING DRAFT
SEQUENCE, 15 unordered pieces.

```

```

ACCESSION AP003043
VERSION AP003043.1 GI:11862945
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE Homo sapiens DNA, clone:RP11-617B3.
ORGANISM Homo sapiens

```

```

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

```

REFERENCE 1 (bases 1 to 180709)

AUTHORS Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P., Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.

TITLE Homo sapiens 180,709 genomic DNA of 11q

JOURNAL Published Only in DataBase (2000) In press

REFERENCE 2 (bases 1 to 180709)

AUTHORS Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P., Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.

TITLE Direct Submission

JOURNAL Submitted (12-DEC-2000) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:hattori@gscc.riken.go.jp, URL:http://hgp.gscc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)

COMMENT

```

----- Genome Center
Center: RIKEN Genomic Sciences Center(GSC)
Center code: RIKEN
Web site: http://hgp.gscc.riken.go.jp/
Contact: hattori@gscc.riken.go.jp
----- Project Information
Center project name: HumDrafit1
Center clone name: RP11-617B3
----- Summary Statistics
Sequencing vector: PCR products; 100% of reads
Chemistry: Dye-terminator ET-amersham; 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 177736 bases at least Q40
Consensus quality: 178788 bases at least Q30
Consensus quality: 179187 bases at least Q20
Insert size: 179309; sum-of-contigs
Quality coverage: 8.67x in Q20 bases; sum-of-contigs

```

NOTE: This is a 'working draft' sequence. It currently consists of 15 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved

1 34592 contig of 34592 bp in length
 34693 58129 contig of 23437 bp in length
 58230 76694 contig of 18465 bp in length
 76795 96488 contig of 19694 bp in length
 96589 110977 contig of 14389 bp in length
 111078 124491 contig of 13414 bp in length
 124592 137310 contig of 12719 bp in length
 137411 148870 contig of 11460 bp in length
 148971 156231 contig of 7261 bp in length
 156332 159291 contig of 2960 bp in length
 159392 185618 contig of 6227 bp in length
 185719 170537 contig of 4819 bp in length
 170638 175407 contig of 4770 bp in length
 175508 179193 contig of 3686 bp in length
 179294 180709 contig of 1416 bp in length.
 * NOTE: This is a 'working draft' sequence. It currently
 * consists of 15 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.

1 34592: contig of 34592 bp in length
 34693 34692: gap of 100 bp
 34693 58129: contig of 23437 bp in length
 58130 58229: gap of 100 bp
 58230 76694: contig of 18465 bp in length
 76695 76794: gap of 100 bp
 76795 96488: contig of 19694 bp in length
 96489 96588: gap of 100 bp
 96589 110977: contig of 14389 bp in length
 110978 111077: gap of 100 bp
 111078 124491: contig of 13414 bp in length
 124492 124591: gap of 100 bp
 124592 137310: contig of 12719 bp in length
 137311 137410: gap of 100 bp
 137411 148870: contig of 11460 bp in length
 148871 148970: gap of 100 bp
 148971 156231: contig of 7261 bp in length
 156232 156331: gap of 100 bp
 156332 159291: contig of 2960 bp in length
 159292 159391: gap of 100 bp
 159392 165618: contig of 6227 bp in length
 165619 165718: gap of 100 bp
 165719 170537: contig of 4819 bp in length
 170538 170637: gap of 100 bp
 170638 173407: contig of 4770 bp in length
 173408 175507: gap of 100 bp
 175508 179193: contig of 3686 bp in length
 179194 179293: gap of 100 bp
 179294 180709: contig of 1416 bp in length.

FEATURES

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 /db_xref="taxon:9606"
 /chromosome="11"
 /map="11q"
 /clone="RP11-617B3"
 1. .34592
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 34693. .58129
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 58230. .76694
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 76795. .96488
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 96589. .110977
 /note="assembly_fragment clone_end:SP6 vector_side:right"
 111078. .124491
 /note="assembly_fragment"
 124592. .137310
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 misc_feature 165719. .170537
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 misc_feature 175508. .179193
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 misc_feature 179294. .180709
 /note="assembly_fragment"

BASE COUNT 56284 a 33949 c 34829 g 54247 t 1400 others
 ORIGIN

alignment_scores:
 Quality: 409.00 Length: 73
 Ratio: 5.603 Gaps: 0
 Percent Similarity: 100.000. Percent Identity: 100.000

alignment_block:

US-09-662-783-4 x AP003043/rev ..
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 20 ValAspLeuAspArgLeuAsnAspAlaLysArgTyrSerCysThrPr 36
 167097 GTTGACCTGGATAGCTCAATGATGATGCAAGCGTTACAGTTCACCTCC 167048
 36 OArgAsnTyrSerValAsnIleArgGluLeuLysLeuAlaAsnVal 53
 167047 CAGGAATTACTCGGTCAATATAAGAGAAGAGCTGAAGTTGCCCAATGTGG 166998
 53 alPhePheProArgCysLeuLeuValGlnArgCysGlyGlyAsnCysGly 69
 166997 TCCTCTTCCACGTTCCCTCCTCGTCAGCGCTGTGGAGGAATTTGGC 166948
 70 CysGlyThrValAsnTrpArgSerCysThrCysAsnSerGlyLysThrVa 86
 166947 TGTGGAACGTCAACTGGAGGTCTTCACATGCAATTCAGGAAACCGT 166898
 86 lLysLysTyrHisGluVal 92
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seq_name: gb_hcg9:AC024052

seq_documentation_block:
 LOCUS AC024052 182403 bp DNA 17-AUG-2000
 DEFINITION Homo sapiens chromosome 11 clone RP11-617B3, WORKING DRAFT
 SEQUENCE 7 unordered pieces.
 ACCESSION AC024052
 VERSION AC024052.3 GI:9838295
 KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.
 SOURCE human.

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 182403)
 AUTHORS Waterston,R.H.
 TITLE The sequence of Homo sapiens clone
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 182403)
 AUTHORS Waterston,R.H.
 TITLE Direct Submission
 JOURNAL Submitted (20-FEB-2000) Genome Sequencing Center, Washington
 University School of Medicine, 4444 Forest Park Parkway, St. Louis,
 MO 63108, USA

COMMENT

On Aug 17, 2000 this sequence version replaced gi:7109658.

----- Genome Center -----
 Center: Washington University Genome Sequencing Center
 Center code: WUGSC
 Web site: http://genome.wustl.edu/gsc/index.shtml
 ----- Project Information -----
 Center project name: H_NH0617B03
 ----- Summary Statistics -----
 Sequencing vector: M13; 100%
 Chemistry: Dye-primer ET; 100% of reads
 Assembly: Dye-terminator Big Dye; 0% of reads
 Assembly program: Phrap; version 0.990319
 Consensus quality: 178574 bases at least Q40
 Consensus quality: 179480 bases at least Q30
 Consensus quality: 179940 bases at least Q20
 Insert size: 198000; agarose-fp
 Insert size: 183143; sum-of-contigs
 Quality coverage: 5.39 in Q20 bases; agarose-fp
 Quality coverage: 5.87 in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently
 * consists of 7 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.

1 1666: contig of 1666 bp in length
 * 1667 1766: gap of unknown length
 * 1767 9133: contig of 7367 bp in length
 * 9134 9233: gap of unknown length
 * 9234 20663: contig of 11430 bp in length
 * 20664 20763: gap of unknown length
 * 20764 35927: contig of 15164 bp in length
 * 35928 36028: gap of unknown length
 * 36028 61610: contig of 25583 bp in length
 * 61611 61710: gap of unknown length
 * 61711 96167: contig of 34457 bp in length
 * 96168 96267: gap of unknown length
 * 96268 182403: contig of 86136 bp in length.

FEATURES

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 /db_xref="taxon:9606"
 /chromosome="11"
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 misc_feature 1767..9133
 /note="assembly_name:Contig3"
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 vector_side:left
 9234..20663
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 misc_feature 36028..61610
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 BASE COUNT 55923 a 35190 c 34519 g 56169 t 602 others
 ORIGIN

alignment_scores:

Quality: 409.00 Length: 73

Ratio: 5.603 Gaps: 0
 Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-662-783-4 x AC024052/rev

Align seg 1/1 to reverse of: AC024052 from: 1 to: 182403

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 |||||
 154066 GTTACCTGGATAGGCTCAATGATGATGCCAAGCGTTACAGTTGCACCTCC 154017
 |||||
 36 oArgAsnTyrSerValAsnIleArgGluLeuLysLeuAlaAsnValV 53
 |||||
 154016 CAGGAATTACTCGGTCAATATAAGAGAAGAGCTGAAGTTGGCCAATGTGG 153967
 |||||
 53 alPhePheProArgCysLeuLeuValGlnArgCysGlyGlyAsnCysGly 69
 |||||
 153966 TCTTCTTTCCACGTTGCCTCCTCGTCGACGCTGTGGAGGAAATTTGTGCG 153917
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 70 CysGlyThrValAsnTyrArgSerCysThrCysAsnSerGlyLysThrVa 86
 |||||
 153916 TGTGGAAGTATCATGAGGTA 153848
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 86 lLysLysTyrHisGluVal 92
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seq_name: gb_ov:AB033829

seq_documentation_block:

LOCUS AB033829 1675 bp mRNA VRT 26-JUL-2000
 DEFINITION Gallus gallus SCDGF mRNA for spinal cord-derived growth factor,
 complete cds.
 ACCESSION AB033829
 VERSION AB033829.1 GI:9392291
 KEYWORDS spinal cord-derived growth factor; scdGF gene.
 SOURCE Gallus gallus (strain:white leghorn) embryo spinal cord cDNA to
 mRNA.

ORGANISM Gallus gallus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
 Phasianinae; Gallus.

REFERENCE

AUTHORS Hamada,T., Ui-Tei,K. and Miyata,Y.
 TITLE A novel gene derived from developing spinal cords, SCDGF, is a
 unique member of the PDGF/VEGF family(1)
 JOURNAL FEBS Lett. 475 (2), 97-102 (2000)
 MEDLINE 20317014
 REFERENCE 2 (bases 1 to 1675)
 AUTHORS Hamada,T., Ui-Tei,K. and Miyata,Y.
 TITLE Direct Submission
 JOURNAL Submitted (25-OCT-1999) to the DDBJ/EMBL/GenBank databases.
 Tsuyoshi Hamada, Nippon Medical School, Department of Pharmacology;
 1-1-5, Sendagi, Bunkyo-ku, Tokyo 113-8602, Japan
 (E-mail:t-hamada@nms.ac.jp, Tel:81-3-3822-2131(ex.5277),
 Fax:81-3-5814-1684)

FEATURES

Location/Qualifiers
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 /strain="white leghorn"
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 /tissue_type="spinal cord"
 103..1140
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 103..1140
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 /translation="MLLGLLLLTSLAGRHHGAAAEEDLSKSFSPFGAQQGVQDP"

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/db_xref="taxon:9606"
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ORIGIN

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Percent Similarity: 76.562 Percent Identity: 49.219

alignment_block:

US-09-662-783-4 x AX028032 ..

Align seg 1/1 to: AX028032 from: 1 to: 1035

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643 CTATATAGGCCCACTTGGCAACTTCTTGGCAAGGCTTTGTTTGGGAAG 692

16 glysSerLys...ValAspLeuAspArgLeuAsnAspAlaLysArgT 32
   | | | | | | | | | | | | | | | | | | | | | | | |
693 AAATCCAGAGTGGTGATCTGAACCTTCTAACAGAGGAGGTAAATAT 742:
   | | | | | | | | | | | | | | | | | | | | | | | |
32 yrSerCysThrProArgAsnTyrSerValAsnIleArgGluLeuLys 48
   | | | | | | | | | | | | | | | | | | | | | | | |
743 ACAGCTGCACACCTCGTAACCTCTCAGTGTCCATAAGGGAAGAACTAAAG 792
   | | | | | | | | | | | | | | | | | | | | | | | |
49 LeuAlaAsnValValPheProArgCysLeuLeuValGlnArgCysG1 65
   ::::| | | | | | | | | | | | | | | | | | | | | | | |
793 AGAACCGGATACCATTTCTGGCCAGGTTGTCTCTGTTAAACCGTGTGG 842
   | | | | | | | | | | | | | | | | | | | | | | | |
65 yGlyAsnCysGlyCysGlyThrValAsnTrpArgSerCysThrCysAsnS 82
   | | | | | | | | | | | | | | | | | | | | | | | |
843 TGGGACTGTGCTGTCTTCTCCACAATTCGAATGCAATGTCATGTGTCC 892

82 erGlyLysThrValLysLysTyrHisGluValLeuGlnPheGluProGly 98
   ::::| | | | | | | | | | | | | | | | | | | | | | | |
893 CAAGCAAGTTACTAAAAAATACCACGAGGTCCTTCAGTTGAGACCA... 939
   | | | | | | | | | | | | | | | | | | | | | | | |
99 HisIleLysArgArgGlyArgAlaLysThrMetAlaLeuValAspIleG1 115
   | | | | | | | | | | | | | | | | | | | | | | | |
940 .....AAGACCGGTGTCCAGGGGATTCACAAATCACCACCGAGTGGC 983

115 nLeuAspHisHisGluArgCysAspCysIleCys 126
   | | | | | | | | | | | | | | | | | | | | | | | |
984 CTGGAGCACCACATGAGGAGTGTGACTGTGTGTGC 1017

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```

715 ATGATATCTGGACACCCCTCGGTATCGAGGCGAGTACATACCATGACCCGAA 764
17 sSerLysValAspLeuAspArgLeuAsnAspAlaLysArgTyrSerC 34
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765 GTCAAAGATTGACCTGGATAGCTCAATGATGATGCCAAGCGTTACAGTT 814
34 ysThrProArgAsnTyrSerValAsnIleArgGluGluLeuLysLeuAla 50
|||||
815 GCACCTCCAGCAATTAATCTCGGTCAATATAAGAGAAGAGCTGAAGTTGGCC 864
51 AsnValValPhePheProArgCysLeuValGlnArgCysGlyGlyAs 67
|||||
865 AATGTGGTCTTCTTCCACGTGGCTCTCTCGTGCAGCGCTGTGAGAGAA 914
67 nCysGlyCysGlyThrValAsnTyrArgSerCysThrCysAsnSerGlyL 84
|||||
915 TTGTGGCTGTGGAATCTCACTGGAGGTCTGCACATGCATTCAGGGA 964
84 ysThrValLysLysTyrHisGluValLeuGlnPheGluProGlyHisIle 100
|||||
965 AAACCGGTGAAGAAGTATCATGAGGTATATACAGTTGTGAGCTGGCCACATC 1014
101 LysArgArgGlyArgAlaLysThrMetAlaLeuValAspIleGlnLeuAs 117
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1015 AAGAGGAGGGGTAGAGCTAAGACCATGGCTCTAGTTGACATCCAGTTGGA 1064
117 pHisHisGluArgCysAspCysIleCysSerSerArgProProArg 132
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seq_documentation_block:
ID AAC81555 standard; cDNA; 1882 BP.

AC AAC81555;
XX
XX 09-MAR-2001 (first entry)
XX
DE Human growth factor homologue zvegf4 cDNA, SEQ ID NO:1.

XX Human; zvegf4; growth factor homologue; VEGF/PDGF family;
KW CUB domain; PDGF-like activity; mitogenic; osteogenic;
KW neovascularisation; tissue repair; proliferation; differentiation;
KW liver damage; neurodegenerative; Alzheimer's disease; multiple sclerosis;
KW periodontal disease; bone fracture; wound healing; vulnerability; ischaemia;
KW immunomodulation; hepatic; chromosome 11q22.3-23.1; ss.
XX
XX Homo sapiens.
OS
XX WO200066736-A1.
PN
XX 09-NOV-2000.
XX
XX 03-MAY-2000; 2000NO-US40047.
PF
XX 03-MAY-1999; 99US-0304216.
PR 10-NOV-1999; 99US-0164463.
PR 04-FEB-2000; 2000US-0180169.
XX
XX (ZYMO) ZYMOGENETICS INC.
PA
XX Gilbert T, Hart CE, Sheppard PO, Gilbertson DG;
PI
XX WPI; 2000-687541/67.
DR P-PSDB; AAB48653.
XX

XX Growth factor homologs and the nucleic acids that encode them, useful
PT e.g. for treating liver damage, ischemia, multiple sclerosis and
PT Alzheimer's disease -
XX
XX Claim 35; Page 106-110; 143pp; English.

CC The invention relates to the human growth factor homologue zvegf4
CC (AAB48653), and nucleic acids encoding it (AAC81555). Zvegf4 is a member
CC of the PDGF (platelet-derived growth factor)/VEGF (vascular endothelial
CC growth factor) family. Zvegf4 has a growth factor domain (AAB48654)
CC characterised by a PDGF cysteine knot structure, and a CUB domain
CC (AAB48655) which has a beta barrel structure. Zvegf4 has PDGF-like
CC activity, having mitogenic activity on fibroblasts, vascular smooth
CC muscle cells and pericytes, and has also been shown to stimulate bone
CC growth. The invention also relates to fusion proteins comprising human
CC zvegf4 or fragments thereof, particularly human zvegf4/human zvegf3
CC fusions; expression constructs and host cells comprising human zvegf4
CC nucleic acids; the recombinant expression of human zvegf4; an antibody
CC which binds to human zvegf4 or a fragment thereof; a method of activating
CC a cell-surface PDGF receptor using a zvegf4-derived polypeptide; a
CC method of modulating the proliferation, differentiation, migration or
CC metabolism of bone cells, comprising exposing bone cells to
CC zvegf4-derived polypeptides; and a method of detecting a genetic
CC abnormality in the zvegf4 gene of a patient. Zvegf4 proteins and derived
CC fragments may be used to stimulate tissue development or repair, or
CC cellular differentiation or proliferation. They are particularly used for
CC the treatment or repair of liver damage, and may also be used to
CC modulate neurite growth (e.g., in the treatment of Alzheimer's disease or
CC multiple sclerosis). Due to their osteogenic activity, they may be used
CC in the treatment of periodontal disease and fractures. They may also be
CC used to enhance expansion and mobilisation of haematopoietic stem cells
CC and endothelial precursor stem cells, which may be useful in the
CC treatment of ischaemia, in wound healing, and in the modulation of the
CC immune system. The present sequence represents cDNA encoding human
CC zvegf4.
XX
SQ Sequence 1882 BP; 566 A; 407 C; 430 G; 479 T; 0 other;

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Quality: 737.00 Length: 132
Ratio: 5.583 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000
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US-09-662-783-4 x AAC81555 ..
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1 MetTyrLeuAspThrProArgTyrArgGlyArgSerTyrHisAspArgLyl 17
940 ATGTATCTGGACACCCCTCGGTATCGAGGCGAGTCTATACCATGACCCGAA 989
17 sSerLysValAspLeuAspArgLeuAsnAspAlaLysArgTyrSerC 34
990 GTCAAAAGTTGACCTGGATAGGCTCAATGATGATGCCAAGCGTTACAGTT 1039
34 ysThrProArgAsnTyrSerValAsnIleArgGluGluLeuLysLeuAla 50
1040 GCACCTCCAGCAATTAATCTCGGTCAATATAAGAGAAGAGCTGAAGTTGGCC 1089
51 AsnValValPhePheProArgCysLeuValGlnArgCysGlyGlyAs 67
1090 AATGTGGTCTTCTTCCACGTGGCTCTCTCGTGCAGCGCTGTGAGAGAA 1139
67 nCysGlyCysGlyThrValAsnTyrArgSerCysThrCysAsnSerGlyL 84
1140 TTGTGGCTGTGGAATCTCACTGGAGGTCTGCACATGCATTCAGGGA 1189
84 ysThrValLysLysTyrHisGluValLeuGlnPheGluProGlyHisIle 100
1190 AAACCGGTGAAGAAGTATCATGAGGTATATACAGTTGTGAGCTGGCCACATC 1239
101 LysArgArgGlyArgAlaLysThrMetAlaLeuValAspIleGlnLeuAs 117
1240 AAGAGGAGGGGTAGAGCTAAGACCATGGCTCTAGTTGACATCCAGTTGGA 1289
117 pHisHisGluArgCysAspCysIleCysSerSerArgProProArg 132
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1290 TCACCATGAACGATCGATTGTATCTGCAGCTCAAGACCACCTCGA 1335

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seq_documentation_block:

ID AAA51541 standard; cDNA; 1882 BP.

XX AC AAA51541;

XX DT 26-SEP-2000 (first entry)

XX DE SEQ. ID. 36 from W00034474.

XX KW Vascular endothelial growth factor; homologue; zvegf3; CUB domain;
KW Cysteine knot; platelet-derived growth factor; PDGF; neuropilin;
KW chromosome 4q28.3; cytostatic; anti-psoriatic; anti-inflammatory;
KW anti-diabetic; ophthalmological; anti-rheumatic; anti-arthritis;
KW vulnery; ss.

XX OS Homo sapiens.

XX PN W0200034474-A2.

XX FH Key Location/Qualifiers
FT CDS 226..1338
FT /*tag= a

XX PD 15-JUN-2000.

XX PF 07-DEC-1999; 99WO-US28968.

XX PR 07-DEC-1998; 98US-0207120.

XX PR 06-JUL-1999; 99US-0142576.

XX PR 21-OCT-1999; 99US-0161653.

XX PR 12-NOV-1999; 99US-0165255.

XX PA (ZYMO) ZYMOGENETICS INC.

XX PI Gao Z, Hart CE, Piddington CS, Sheppard PO, Shoemaker KE;

XX PI Gilbertson DG, West JW;

XX DR WFI; 2000-423420/36.

XX DR P-PSDB; AAY96864.

XX PT Novel zvegf3 polypeptides and nucleotides encoding them useful for

XX PT stimulating growth of smooth muscle cells and fibroblasts comprising an

XX PT epitope bearing portion of a specific amino acid sequence

XX PS Disclosure; Page 161-164; 173pp; English.

XX CC Polypeptides comprising an epitope-bearing portion human or murine
XX CC ZVEGF3 (vascular endothelial growth factor homologue) are claimed. The
XX CC growth factors comprise a growth factor domain and a CUB domain (generic
XX CC sequence motifs are shown in AAY96859 and AAY96860). The growth factor
XX CC domain is characterized by an arrangement of cysteine residues and
XX CC beta-strands that is characteristic of the "cysteine knot" structure of
XX CC the platelet-derived growth factor (PDGF) family. The CUB domain shows
XX CC homology to CUB domains in neuropilins, human bone morphogenetic
XX CC protein-1, porcine seminal plasma protein, bovine acidic seminal fluid
XX CC protein and xenopus laevis tolloid-like protein. Structural analysis and
XX CC homology predict that ZVEGF3 polypeptides complex with a second
XX CC polypeptide to form multimeric proteins. The human zvegf3 gene has been
XX CC mapped to chromosome 4q28.3. ZVEGF3 is useful for stimulating the growth
XX CC of fibroblasts or smooth muscle cells, for activating cell surface
XX CC PDGF-alpha receptor and for inhibiting PDGF-alpha receptor mediated
XX CC cellular processes. ZVEGF3 is useful for regulating (post-development)
XX CC organ growth, regeneration and maintenance, as well as tissue
XX CC maintenance and repair processes. ZVEGF3 antagonists are useful for
XX CC treating cancer, rheumatoid arthritis, diabetic retinopathy, ischemic
XX CC limb disease, peripheral vascular disease, myocardial ischemia, vascular
XX CC intimal hyperplasia, atherosclerosis, wound healing, chronic liver
XX CC disease and haemangioma formation. ZVEGF3 can also be used to modulate
XX CC neurite growth and development of the nervous system, and for treating

CC neurodegenerative diseases.

XX

SQ Sequence 1882 BP; 566 A; 407 C; 430 G; 479 T; 0 other;

alignment_scores:

Quality: 737.00 Length: 132
Ratio: 5.583 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-662-783-4 x AAA51541 ..

Align seg 1/1 to: AAA51541 from: 1 to: 1882

1 MetTyrLeuAspThrProArgTyrArgGlyArgSerTyrHisAspArgly 17

940 ATGTATCTGGACACCCCTCGGTATCGAGCGAGGTATACCATGCCGAA 989

17 sSerLysValAspLeuAspArgLeuAsnAspAlaLysArgTyrSerC 34

990 GTCAAAAGCTTCACCTGGATAGGCTCAATGATCATGCCAAGCGTTACGTT 1039

34 ysThrProArgAsnTyrSerValAsnIleArgGluGluLeuLysLeuAla 50

1040 GCACCTCCAGGAATTAATCTCGGTCAATATAAGAGAAGAGCTGAAGTTGGCC 1089

51 AsnValValPhePheProArgCysLeuValGlnArgCysGlyGlyAs 67

1090 AATGTGGTCTTCTTTCCACGTTGCCTCTCGTGCAGCGCTGTGGAGAAA 1139

67 nCysGlyCysGlyThrValAsnTrpArgSerCysThrCysAsnSerGlyL 84

1140 TTGTGGCTGTGGAAGTCACTGCACTGGAGGTCTGTCACATGCATTCAGGGA 1189

84 ysThrValLysLysTyrHisGluValLeuGlnPheGluProGlyHisIle 100

1190 AAACCGTGAAAGATATCATGAGGTATTACAGTTTGAGCGTGGCCACATC 1239

101 LysArgArgGlyArgAlaLysThrMetAlaLeuValAspIleGlnLeuAs 117

1240 AAGAGGAGGGGTAGAGCTTAAGACCATGGCTCTAGTTGACATCCAGTTGGA 1289

117 pHisHisGluArgCysAspCysIleCysSerSerArgProProArg 132

1290 TCACCATGACGATCGATTGTATCTGCAGCTCAAGACCACCTCGA 1335

seq_name: /SIDS1/gcgdata/geneseq/geneseq/NA2000.DAT: AAD00737

seq_documentation_block:

ID AAD00737 standard; cDNA; 1934 BP.

XX AC AAD00737;

XX DT 08-SEP-2000 (first entry)

XX DE Human Platelet Derived Growth Factor (PDGF)-D encoding partial cDNA #2.

XX KW Platelet Derived Growth Factor-D; PDGF-D; human; cytostatic; vulnery;

XX KW VEGF-G; Vascular Endothelial Growth Factor; antiatherosclerotic; tumour;

XX KW proliferative; activator; proliferation; differentiation; motility;

XX KW growth; PDGF-D receptor; antagonist; tissue remodelling; treat;

XX KW atherosclerosis; wound; metastasis; ss.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

FT CDS 1..969

FT /*tag= a

FT /partial

FT /product= "Human PDGF-D partial polypeptide #2"

FT /note= "5, truncated platelet derived growth factor"

XX

PN WO200027879-A1.
 XX 18-MAY-2000.
 XX 10-NOV-1999; 99WO-US26462.
 XX 10-NOV-1998; 98US-0107852.
 PR 28-DEC-1998; 98US-0113997.
 PR 26-AUG-1999; 99US-0150604.
 PR 04-OCT-1999; 99US-0157108.
 PR 05-OCT-1999; 99US-0157756.
 XX (LUDW-) LUDWIG INST CANCER RES.
 PA (UYHE-) UNIV HELSINKI LICENSING LTD OY.
 XX Eriksson U, Aase K, Ponten A, Lee X, Uutela M, Alitalo K;
 PI Oestman A, Heldin C;
 XX WPI; 2000-376495/32.
 DR P-PSDB; AAY711129.
 XX Novel polynucleotides encoding a novel growth factor of cells
 PT expressing a platelet-derived growth factor, useful for diagnostic and
 PT therapeutic applications, e.g. concerning cancer -
 XX Claim 1; Fig 5; 11pp; English.
 XX The present sequence is the 5' truncated partial cDNA #2, encoding human
 CC platelet derived growth factor (PDGF)-D, formally known as Vascular
 CC Endothelial Growth Factor (VEGF)-G. It is derived from human foetal lung
 CC lamdag10 cDNA library. It belongs to the VEGF/PDGF family. It functions
 CC as an activator of proliferation, differentiation, growth and motility of
 CC cells, that express PDGF-D receptor. This sequence is useful for
 CC inhibiting the growth of tumours, that express PDGF-D. Expression of
 CC PDGF-D and its proteolytic cleavage for generating an activated truncated
 CC PDGF-D antagonist is useful for inhibiting tissue remodelling during the
 CC invasion of tumour cells into normal cells. PDGF-D may be used to treat
 CC wounds, atherosclerosis, metastasis and migration of smooth muscle cells.
 XX Sequence 1934 BP; 632 A; 366 C; 394 G; 542 T; 0 other;
 SQ

alignment_scores:
 Quality: 737.00 Length: 132
 Ratio: 5.583 Gaps: 0
 Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
 US-09-662-783-4 x AAD00737 ..
 Align seg 1/1 to: AAD00737 from: 1 to: 1934
 1 MetTyrLeuAspThrProArgTyrArgGlyArgSerTyrHisAspArgLy 17
 571 ATGTATCTGGACACCCCTCGGTATCGAGGAGGTCATACCATGCCGGA 620
 17 sSerLysValAspLeuAspArgLeuAsnAspAspAlaLysArgTyrSerC 34
 621 GTCAAAAGTTGACCTGGATAGGCTCATGTATGATGCCAAGCGTTACAGTT 670
 34 ysThrProArgAsnTyrSerValAsnTleArgGluGluLeuLysLeuAla 50
 671 GCACCTCCAGGAATTTACTCGGTCAATATAAGAGAAGAGCTGAAGTTGCC 720
 51 AsnValValPhePheProArgCysLeuValGlnArgCysGlyGlyAs 67
 721 AATGTGCTCTTCTTCACCGTGGCTCTCTCGTCAGCGCTGTGGAGAAA 770
 67 nCysGlyCysGlyThrValAsnTrpArgSerCysThrCysAsnSerGlyL 84
 771 TTGTGGCTGTGGAACTGCACTCAACTGGAGTCTCTGCACATGCAATTCAGGA 820

84 ysThrValLysLysTyrHisGluValLeuGlnPheGluProGlyHisIle 100
 821 AAACCGTGAAAAAGTATCATGAGGTATTACAGTTTGGCCTGGCCACATC 870
 101 LysArgArgGlyArgAlaLysThrMetAlaLeuValAspIleGlnLeuAs 117
 871 AAGAGGAGGGGTAGAGCTAAGACCATGGCTCTAGTTGACATCCAGTTGGA 920
 117 pHHisGluArgCysAspCysIleCysSerSerArgProProArg 132
 921 TCACCATGACGATCGATTGTATCTGCAGCTCAAGACCCTCGA 966
 seq_name: /SIDS1/gcgdata/geneseq/geneseq/NA2000.DAT.AAD00738
 seq_documentation_block:
 ID AAD00738 standard; cDNA; 2253 BP.
 XX AAD00738;
 AC AAD00738;
 XX 08-SEP-2000 (first entry)
 DT
 XX Human Platelet Derived Growth Factor (PDGF)-D encoding complete cDNA.
 DE Platelet Derived Growth Factor-D; PDGF-D; human; cytostatic; vulnerary;
 XX VEGF-G; Vascular Endothelial Growth Factor; antiatherosclerotic; tumour;
 KW proliferative; activator; proliferation; differentiation; motility;
 KW growth; PDGF-D receptor; antagonist; tissue remodelling; treat;
 KW atherosclerosis; wound; metastasis; ss.
 XX Homo sapiens.
 OS
 XX Key Location/Qualifiers
 FH 176..1288
 CDS /*tag= a
 FT /product= "human PDGF-D protein"
 FT /note= "Platelet derived growth factor"
 XX WO200027879-A1.
 XX 18-MAY-2000.
 XX 10-NOV-1999; 99WO-US26462.
 XX 10-NOV-1998; 98US-0107852.
 PR 28-DEC-1998; 98US-0113997.
 PR 26-AUG-1999; 99US-0150604.
 PR 04-OCT-1999; 99US-0157108.
 PR 05-OCT-1999; 99US-0157756.
 XX (LUDW-) LUDWIG INST CANCER RES.
 PA (UYHE-) UNIV HELSINKI LICENSING LTD OY.
 XX Eriksson U, Aase K, Ponten A, Lee X, Uutela M, Alitalo K;
 PI Oestman A, Heldin C;
 XX WPI; 2000-376495/32.
 DR P-PSDB; AAY711130.
 XX Novel polynucleotides encoding a novel growth factor of cells
 PT expressing a platelet-derived growth factor, useful for diagnostic and
 PT therapeutic applications, e.g. concerning cancer -
 XX Claim 1; Fig 7; 11pp; English.
 XX The present sequence is the complete cDNA encoding human platelet derived
 CC growth factor (PDGF)-D, formally known as Vascular Endothelial Growth
 CC Factor (VEGF)-G. It is derived from human foetal lung lamda g10 cDNA
 CC library. It belongs to the VEGF/PDGF family. It functions as an activator
 CC of proliferation, differentiation, growth and motility of cells, that
 CC express PDGF-D receptor. This sequence is useful for inhibiting the
 CC growth of tumours, that express PDGF-D. Expression of PDGF-D and its
 CC proteolytic cleavage for generating an activated truncated form is useful
 CC for regulating receptor binding specificity of PDGF-D. PDGF-D antagonist

CC is useful for inhibiting tissue remodelling during the invasion of
 CC tumour cells into normal cells. PDGF-D may be used to treat wounds,
 CC atherosclerosis, metastasis and migration of smooth muscle cells.
 XX
 SQ Sequence 2253 BP; 701 A; 464 C; 490 G; 598 T; 0 other;

alignment_scores:
 Quality: 737.00 Length: 132
 Ratio: 5.583 Gaps: 0
 Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-662-783-4 x AAD00738 ..

Align seg 1/1 to: AAD00738 from: 1 to: 2253

1 MetTyrLeuAspThrProArgTyrArgGlyArgSerTyrHisAspArgly 17
 |||||
 890 ATGTATCTGGACACCCCTCGGTATCGAGCGAGTCCATACCATGACCGAA 939
 |||||
 17 sSerLysValAspLeuAspArgLeuAsnAspAlaLysArgTyrSerC 34
 |||||
 940 GTCAAAAGTTGACCTGGATAGGCTCAATGATGATGCCAAGCGTTACAGTT 989
 |||||
 34 ysThrProArgAsnTyrSerValAsnIleArgGluGluLeuLysLeuAla 50
 |||||
 990 GCACCTCCAGGAATTTACTCGGTCAATATAGAGAGAGCTGAAGTTGGCC 1039
 |||||
 51 AsnValValPhePheProArgCysLeuLeuValGlnArgCysGlyGlyAs 67
 |||||
 1040 AATGTGGTCTTCTTCCACGTTGCTCGCTCGTCGACGCGCTGTGGAGAA 1089
 |||||
 67 nCysGlyCysGlyThrValAsnTrpArgSerCysThrCysAsnSerGlyL 84
 |||||
 1090 TTGTGGCTGTGAAGTGTCACTGGAGGTCCTGCACATGCAATTCAGGGA 1139
 |||||
 84 ysThrValLysLysTyrHisGluValLeuGlnPheGluProGlyHisIle 100
 |||||
 1140 AAACCGTGAAGAATATCATGAGGTATTACAGTTTGAGCCTGGCCACATC 1189
 |||||
 101 LysArgArgGlyArgAlaLysThrMetAlaLeuValAspIleGlnLeuAs 117
 |||||
 1190 AAGAGAGGGGTAGAGCTAAGACCATGGCTCTAGTTGACATCCAGTTGGA 1239
 |||||
 117 phisHisGluArgCysAspCysIleCysSerSerArgProProArg 132
 |||||
 1240 TCACCATGAACGATGCGATTGTATGTGACGCTCAAGACCCACCTCGA 1285

seq_name: /SIDS1/gcgdata/geneseq/geneseq/NA2001.DAT:AAF24196

seq_documentation_block:

ID AAF24196 standard; DNA; 3853 BP.

XX AAF24196;

DT 02-APR-2001 (first entry)

DE Human VEGF-G cDNA.

XX Vascular endothelial growth factor; VEGF; cancer; cell;
 KW angiogenesis; ss.

OS Homo sapiens.

XX WO200100878-A2.

PN 04-JAN-2001.

XX 29-JUN-2000; 2000WO-US18085.

XX 30-JUN-1999; 99US-0343671.

XX

PA (MILL-) MILLENNIUM PHARM INC.

XX Gearing DP;

XX WPI; 2001-050129/06.

XX New vascular endothelial growth factor family member used for diagnosis
 PT and treatment of deregulated cell growth e.g. cancer, disorders
 PT involving aberrant angiogenesis e.g. psoriasis, and chronic
 PT inflammatory diseases -

XX Claim 1; Fig 1; 142pp; English.

XX The present invention relates to a vascular endothelial growth factor
 CC (VEGF) family member, VEGF-G. VEGF-G protein and nucleic acid
 CC molecules are used as modulating agents or as targets for
 CC developing modulating agents to regulate a variety of cellular
 CC processes e.g. cell proliferation, differentiation, migration and
 CC wound repair. VEGF-G modulators, i.e. VEGF-G protein, peptide,
 CC peptidomimetic or nucleic acid are used to treat a subject with
 CC aberrant VEGF-G protein or nucleic acid expression or activity
 CC e.g. deregulated cell growth, such as cancer, hyperproliferative bone
 CC disorders, disorders involving aberrant angiogenesis e.g. psoriasis,
 CC and chronic inflammatory diseases e.g. rheumatoid arthritis. VEGF-G
 CC gene expression is inhibited through the administration of antisense
 CC molecules or ribozymes and by targeting the regulatory region of VEGF-G
 CC to prevent transcription of the gene in target cells.

XX Sequence 3853 BP; 1194 A; 771 C; 757 G; 1131 T; 0 other;

alignment_scores:

Quality: 737.00 Length: 132
 Ratio: 5.583 Gaps: 0
 Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-662-783-4 x AAF24196 ..

Align seg 1/1 to: AAF24196 from: 1 to: 3853

1 MetTyrLeuAspThrProArgTyrArgGlyArgSerTyrHisAspArgly 17
 |||||
 927 ATGTATCTGGACACCCCTCGGTATCGAGCGAGTCCATACCATGACCGAA 976
 |||||
 17 sSerLysValAspLeuAspArgLeuAsnAspAlaLysArgTyrSerC 34
 |||||
 977 GTCAAAAGTTGACCTGGATAGGCTCAATGATGATGCCAAGCGTTACAGTT 1026
 |||||
 34 ysThrProArgAsnTyrSerValAsnIleArgGluGluLeuLysLeuAla 50
 |||||
 1027 GCACCTCCAGGAATTTACTCGGTCAATATAGAGAGAGCTGAAGTTGGCC 1076
 |||||
 51 AsnValValPhePheProArgCysLeuLeuValGlnArgCysGlyGlyAs 67
 |||||
 1077 AATGTGGTCTTCTTCCACGTTGCTCGCTCGTCGACGCGCTGTGGAGAA 1126
 |||||
 67 nCysGlyCysGlyThrValAsnTrpArgSerCysThrCysAsnSerGlyL 84
 |||||
 1127 TTGTGGCTGTGAAGTGTCACTGGAGGTCCTGCACATGCAATTCAGGGA 1176
 |||||
 84 ysThrValLysLysTyrHisGluValLeuGlnPheGluProGlyHisIle 100
 |||||
 1177 AAACCGTGAAGAATATCATGAGGTATTACAGTTTGAGCCTGGCCACATC 1226
 |||||
 101 LysArgArgGlyArgAlaLysThrMetAlaLeuValAspIleGlnLeuAs 117
 |||||
 1227 AAGAGAGGGGTAGAGCTAAGACCATGGCTCTAGTTGACATCCAGTTGGA 1276
 |||||
 117 phisHisGluArgCysAspCysIleCysSerSerArgProProArg 132
 |||||
 1277 TCACCATGAACGATGCGATTGTATGTGACGCTCAAGACCCACCTCGA 1322

seq_name: /SIDS1/gcgdata/geneseq/geneseq/NA2000.DAT:AAD00736

seq_documentation_block:

ID AAD00736 standard; cDNA; 690 BP.

AC AAD00736;

XX 08-SEP-2000 (first entry)

XX Human Platelet Derived Growth Factor (PDGF)-D encoding partial cDNA #1.

XX Platelet Derived Growth Factor-D; PDGF-D; human; cytostatic; vulnery;
 KW VEGF-G; Vascular Endothelial Growth Factor; antiatherosclerotic; tumour;
 KW proliferative; activator; proliferation; differentiation; motility;
 KW growth; PDGF-D receptor; antagonist; tissue remodelling; treat;
 KW atherosclerosis; wound; metastasis; ss.

XX Homo sapiens.

XX Key Location/Qualifiers

FT CDS 1..603

FT /*tag- a

FT /partial

FT /product- "Human PDGF-D partial polypeptide #1"

FT /note- "5' truncated platelet derived growth factor"

XX WO200027879-A1.

XX 18-MAY-2000.

XX 10-NOV-1999; 99WO-US26462.

XX 10-NOV-1998; 98US-0107852.

XX 28-DEC-1998; 98US-0113997.

XX 26-AUG-1999; 99US-0150604.

XX 04-OCT-1999; 99US-0157108.

XX 05-OCT-1999; 99US-0157756.

XX {LUDW-} LUDWIG INST CANCER RES.

XX {UYHE-} UNIV HELSINKI LICENSING LTD OY.

XX Eriksson U, Aase K, Ponten A, Lee X, Uutela M, Alitalo K;

XX Oestman A, Heldin C;

XX WPI; 2000-376495/32.

XX P-PSDB; AA711128.

XX Novel polynucleotides encoding a novel growth factor of cells
 PT expressing a platelet-derived growth factor, useful for diagnostic and
 PT therapeutic applications, e.g. concerning cancer -

XX Claim 1; Fig 3; 111pp; English.

XX The present sequence is the 5' truncated partial cDNA #1, encoding human
 CC platelet derived growth factor (PDGF)-D, formally known as Vascular
 CC Endothelial Growth Factor (VEGF)-G. It is derived from human foetal lung
 CC lambda2g10 cDNA library. It belongs to the VEGF/PDGF family. It functions
 CC as an activator of proliferation, differentiation, growth and motility of
 CC cells, that express PDGF-D receptor. This sequence is useful for
 CC inhibiting the growth of tumours, that express PDGF-D. Expression of
 CC PDGF-D and its proteolytic cleavage for generating an activated truncated
 CC form is useful for regulating receptor binding specificity of PDGF-D.
 CC PDGF-D antagonist is useful for inhibiting tissue remodelling during the
 CC invasion of tumour cells into normal cells. PDGF-D may be used to treat
 CC wounds, atherosclerosis, metastasis and migration of smooth muscle cells.

XX Sequence 690 BP; 202 A; 157 C; 166 G; 165 T; 0 other;

alignment_scores:

Quality: 713.00 Length: 132

Ratio: 5.443 Gaps: 0

Percent Similarity: 99.242 Percent Identity: 97.727

alignment_block:

US-09-662-783-4 x AAD00736

Align seg 1/1 to: AAD00736 from: 1 to: 690

1 MetTyrLeuAspThrProArgTyrArgGlyArgSerTyrHisAspArgly 17
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 205 ATGTATCTGGACACCCCTCGGTATCGAGGAGGTACATACCATGACCGGAA 254

17 sSerLysValAspLeuAspArgLeuAsnAspAlaLysArgTyrSerC 34
 |||||
 255 GTCAAAAGTTGACCTGGATAGGCTCAATGATGATGCCAAGCGTTACAGTT 304

34 ystThrProArgAsnTyrSerValAsnIleArgGluGluLeuLysLeuAla 50
 |||||
 305 GCACCTCCAGGAATTACTCGGTCAATATTAAGAAGAGAGCTGAAGTTGGCC 354

51 AsnValValPhePheProArgCysLeuValGlnArgCysGlyGlyAs 67
 |||||
 355 AATGTGTCTTCTTTCCACGTTGCCTCCTCGTCGACGCGCTGTGGAGGAA 404

67 nCysGlyCysGlyThrValAsnTrpArgSerCysThrCysAsnSerGlyL 84
 |||||
 405 TTGTGGCTGTGGAATGTCAAACTGGAGTCTCTGCACATGCAATTCAGGGA 454

84 ystThrValLysTyrHisGluValLeuGlnPheGluProGlyHisIle 100
 |||||
 455 AAACCGTGAAAAGATATCATGAGGTATTACAGTTTGAGCCTGGCCACATC 504

101 LysArgArgGlyArgAlaLysThrMetAlaLeuValAspIleGlnLeuAs 117
 |||||
 505 AAGAGGAGGGGTAGAGCTAAGACCATGGCTCTAGTTGACATCCAGTTGGA 554

117 pHisHisGluArgCysAspCysIleCysSerSerArgProProArg 132
 |||||
 555 TCACCATGAACGATGCGATTGTATCTGCAGCTCAAGACCACTCGA 600

seq_name: /SIDS1/gcgdata/geneseq/geneseq/NA2000.DAT:AAC81596

seq_documentation_block:

ID AAC81596 standard; DNA; 1472 BP.

XX AC AAC81596;

XX AC

XX DT 09-MAR-2001 (first entry)

XX DE Mouse growth factor homologue zveg4 DNA, SEQ ID NO:52.

XX KW Mouse; murine; zveg4; growth factor homologue; VEGF/PDGF family;
 KW CUB domain; PDGF-like activity; mitogenic; osteogenic;
 KW neovascularisation; tissue repair; proliferation; differentiation;
 KW liver damage; neurodegenerative; Alzheimer's disease; multiple sclerosis;
 KW periodontal disease; bone fracture; wound healing; ischaemia;
 KW immunomodulation; hepatic; ds.

XX OS Mus musculus.

XX PN WO200066736-A1.

XX PD 09-NOV-2000.

XX PF 03-MAY-2000; 2000WO-US40047.

XX PR 03-MAY-1999; 99US-0304216.

XX PR 10-NOV-1999; 99US-0164463.

XX PR 04-FEB-2000; 2000US-0180169.

XX PA (ZYMO) ZYMOGENETICS INC.

XX PI Gilbert T, Hart CE, Sheppard PO, Gilbertson DG;

XX DR WPI; 2000-687541/67.

DR P-PSDB; AAB48663.
XX Growth factor homologs and the nucleic acids that encode them, useful
PT e.g. for treating liver damage, ischemia, multiple sclerosis and
PT Alzheimer's disease.
XX
XX Example 19; Page 136-138; 143pp; English.
PS
CC The invention relates to the human growth factor homologue zvegfg
CC (AAB48653), and nucleic acids encoding it (AAC81555). Zvegfg is a member
CC of the PDGF (platelet-derived growth factor)/VEGF (vascular endothelial
CC growth factor) family. Zvegfg has a growth factor domain (AAB48654)
CC characterised by a PDGF cysteine knot structure, and a CUB domain
CC (AAB48655) which has a beta barrel structure. Zvegfg has PDGF-like
CC activity, having mitogenic activity on fibroblasts, vascular smooth
CC muscle cells and pericytes, and has also been shown to stimulate bone
CC growth. The invention also relates to fusion proteins comprising human
CC zvegfg or fragments thereof, particularly human zvegfg4/human zvegfg3
CC fusions; expression constructs and host cells comprising human zvegfg
CC nucleic acids; the recombinant expression of human zvegfg4; an antibody
CC which binds to human zvegfg4 or a fragment thereof; a method of activating
CC a cell-surface PDGF receptor using a zvegfg4-derived polypeptide; a
CC method of modulating the proliferation, differentiation, migration or
CC metabolism of bone cells, comprising exposing bone cells to
CC zvegfg4-derived polypeptides; and a method of detecting a genetic
CC abnormality in the zvegfg4 gene of a patient. Zvegfg4 proteins and derived
CC fragments may be used to stimulate tissue development or repair, or
CC cellular differentiation or proliferation. They are particularly used for
CC the treatment or repair of liver damage, and may also be used to
CC modulate neurite growth (e.g., in the treatment of Alzheimer's disease or
CC multiple sclerosis). Due to their osteogenic activity, they may be used
CC in the treatment of periodontal disease and fractures. They may also be
CC used to enhance expansion and mobilisation of haematopoietic stem cells
CC and endothelial precursor stem cells; which may be useful in the
CC treatment of ischaemia, in wound healing, and in the modulation of the
CC immune system. The present sequence represents DNA encoding mouse
CC zvegfg4.
XX
XX Sequence 1472 BP; 434 A; 327 C; 332 G; 379 T; 0 other;

alignment_scores:

Quality: 686.00 Length: 132
Ratio: 5.197 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 90.152

alignment_block:

US-09-662-783-4 x AAC81596

Align seg 1/1 to: AAC81596 from: 1 to: 1472

1 MetTyrLeuAspThrProArgTyrArgGlyArgSerTyrHisAspArgly 17
807 TTGTATCTGGACACCCCTCATATAGAGCGAGGTATACCATGATCGGAA 856
17 sSerTysValAspLeuAspArgLeuAsnAspAlaLysArgTyrSerC 34
857 GTCCAAAGTGGACCTGGACAGGCTCAATCATGTCATGTCAGGCTTACAGTT 906
34 yThrProArgAsnTyrSerValAsnIleArgGluLeuLeuLysLeuAla 50
907 GCACCTCCACAGGAATCACTGTGTGAACCTCAGGAGGAGCTGAAGCTGACC 956
51 AsnValValPhePheProArgCysLeuLeuValGlnArgCysGlyGlyAs 67
957 AATGCAGTCTTCTTCCAGAGTCCCTCCGTCGACGCTGTGGTGCA 1006
67 nCysGlyCysGlyThrValAsnTrpArgSerCysThrCysAsnSerGlyL 84
1007 CTGTGGTTCGGAACACTGTCAACTGGAAGTCTGCACATCAGCTCAGGCA 1056
84 yThrValLysTyrTyrHisGluValLeuGlnPheGluProGlyHisIle 100
|||||

1057 AGACAGTGAAGAAGTATCATGAGGTATTGAAGTTTGAGCTGGACATTTC 1106
101 LysArgArgGlyArgAlaLysThrMetAlaLeuValAspIleGlnLeuAs 117
|||||
1107 AAGAGAAGGGCAAGCTAAGAATATGCTCTTGTGTATATCCAGCTGGA 1156
117 phishHisGluArgCysAspCysIleCysSerSerArgProProArg 132
|||||
1157 TCATCATGAGCGATGCTACTGTATCTGTCAGCTCAAGACCCACCTCGA 1202
seq_name: /SIDS1/gcdata/geneseq/geneseqn/NA2001.DAT:AAF24199
seq_documentation_block:
ID AAF24199 standard; DNA; 1110 BP.
XX
AC AAF24199;
XX
DT 02-APR-2001 (first entry)
XX
DE Human VEGF-G coding region.
XX
KW Vascular endothelial growth factor; VEGF; cancer; cell;
KW angiogenesis; ss.
XX
OS Homo sapiens.
XX
PN WC200100878-A2.
XX
PD 04-JAN-2001.
XX
PF 29-JUN-2000; 2000WO-US18085.
XX
PR 30-JUN-1999; 99US-0343671.
XX
PA (MILL-) MILLENNIUM PHARM INC.
XX
PI Gearing DP;
XX
DR WPI; 2001-050129/06.
XX
PT New vascular endothelial growth factor family member used for diagnosis
PT and treatment of deregulated cell growth e.g. cancer, disorders
PT involving aberrant angiogenesis e.g. psoriasis, and chronic
PT inflammatory diseases.
XX
PS Claim 1; Fig 8; 142pp; English.
XX
CC The present invention relates to a vascular endothelial growth factor
CC (VEGF) family member, VEGF-G. VEGF-G protein and nucleic acid
CC molecules are used as modulating agents or as targets for
CC developing modulating agents to regulate a variety of cellular
CC processes e.g. cell proliferation, differentiation, migration and
CC wound repair. VEGF-G modulators, i.e. VEGF-G protein, peptide,
CC peptidomimetic or nucleic acid are used to treat a subject with
CC aberrant VEGF-G protein or nucleic acid expression or activity
CC e.g. deregulated cell growth, such as cancer, hypertrophic bone
CC disorders, disorders involving aberrant angiogenesis e.g. psoriasis,
CC and chronic inflammatory diseases e.g. rheumatoid arthritis. VEGF-G
CC gene expression is inhibited through the administration of antisense
CC molecules or ribozymes and by targeting the regulatory region of VEGF-G
CC to prevent transcription of the gene in target cells.
XX
SQ Sequence 1110 BP; 313 A; 267 C; 269 G; 261 T; 0 other;

alignment_scores:

Quality: 681.00 Length: 132
Ratio: 5.198 Gaps: 0
Percent Similarity: 99.242 Percent Identity: 89.394

alignment_block:

US-09-662-783-4 x AAF24199

Align seg 1/1 to: AAF24199 from: 1 to: 1110

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1 MetTyrLeuAspThrProArgTyrArgGlyArgSerTyrHisAspArgLy 17
:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
715 TTGTATCTGGACACCCCTCATATATAGAGGACAGTCATACCATGATCGGAA 764

17 sSerLysValAspLeuAspArgLeuAsnAspAspAlaLysArgTyrSerC 34
|||||:::|||||:::|||||:::|||||:::|||||:::|||||
765 GTCCAAAGTGGACCTGGACAGGCTCAATGATGATGATCAAGCGTTACAGTT 814

34 yThrProArgAsnTyrSerValAsnLeuArgGluGluLeuLysLeuAla 50
|||||:::|||||:::|||||:::|||||:::|||||:::|||||
815 GCATCTCCAGGAATCACTCTGTGAACCTCAGGAGAGCTGAAGCTGACC 864

51 AsnValValPhePheProArgCysLeuValGlnArgCysGlyGlyAs 67
|||||:::|||||:::|||||:::|||||:::|||||:::|||||
865 ANTGCAGTCTTCTCCACAGATGCTCTCTGTGACGCGCTGTGTGGCAA 914

67 nCysGlyCysGlyThrValAsnTrpArgSerCysThrCysAsnSerGlyL 84
|||||:::|||||:::|||||:::|||||:::|||||:::|||||
915 CTGTGTTGGCGAACTGTCAACTGGAAGTCTGCACATGCAGCTCAGGGA 964

84 yThrValLysLysTyrHisGluValLeuGlnPheGluProGlyHisLe 100
|||||:::|||||:::|||||:::|||||:::|||||:::|||||
965 AGACAGTGAAGAAGTATCACAGAGTATTGAAGTTGAGCCTGGACATTC 1014

101 LysArgArgGlyArgAlaLysThrMetAlaLeuValAspLeuGlnLeu 117
:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
1015 AAGAGAGGGGCAAGCTAGAAATATGCCCTCTTGTGATATCCAGCTGGA 1064

117 pHISHisGluArgCysAspCysIleCysSerSerArgProProArg 132
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1065 TCATCATGAGCGATGTGACTGTATCTGACGCTCAAGACCACCTCGA 1110

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seq_name: /SIDS1/gcgdata/geneseq/geneseq/NA2001.DAT:AAF24198

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seq_documentation_block:
ID  AAF24198 standard; DNA; 3121 BP.
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AC  AAF24198;
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DT  02-APR-2001 (first entry)
XX
DE  Human VEGF-G cDNA.
XX
KW  Vascular endothelial growth factor; VEGF; cancer; cell;
KW  angiogenesis; ss.
XX
OS  Homo sapiens.
XX
PN  WO200100878-A2.
XX
PD  04-JAN-2001.
XX
PF  29-JUN-2000; 2000WO-US18085.
XX
PR  30-JUN-1999; 99US-0343671.
XX
PA  (MILL-) MILLENNIUM PHARM INC.
XX
PI  Gearing DP;
XX
WPI; 2001-050129/06.
XX
PT  New vascular endothelial growth factor family member used for diagnosis
PT  and treatment of deregulated cell growth e.g. cancer, disorders
PT  involving aberrant angiogenesis e.g. psoriasis, and chronic
PT  inflammatory diseases -
XX
PS  Claim 1; Fig 8; 142pp; English.
XX
CC  The present invention relates to a vascular endothelial growth factor
CC  (VEGF) family member, VEGF-G. VEGF-G protein and nucleic acid

```

CC molecules are used as modulating agents or as targets for developing modulating agents to regulate a variety of cellular processes e.g. cell proliferation, differentiation, migration and wound repair. VEGF-G modulators, i.e. VEGF-G protein, peptide, peptidomimetic or nucleic acid are used to treat a subject with aberrant VEGF-G protein or nucleic acid expression or activity e.g. deregulated cell growth, such as cancer, hyperproliferic bone disorders, disorders involving aberrant angiogenesis e.g. psoriasis, and chronic inflammatory diseases e.g. rheumatoid arthritis. VEGF-G gene expression is inhibited through the administration of antisense molecules or ribozymes and by targeting the regulatory region of VEGF-G to prevent transcription of the gene in target cells.

XX
SQ Sequence 3121 BP; 980 A; 611 C; 637 G; 893 T; 0 other;

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alignment_scores:
Quality: 681.00      Length: 132
Ratio: 5.198        Gaps: 0
Percent Similarity: 99.242 Percent Identity: 89.394

alignment_block:
US-09-662-783-4 x AAF24198 ..
Align seg 1/1 to: AAF24198 from: 1 to: 3121

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879 TTGTATCTGGACACCCCTCATATATAGAGGACAGTCATACCATGATCGGAA 928

17 sSerLysValAspLeuAspArgLeuAsnAspAspAlaLysArgTyrSerC 34
|||||:::|||||:::|||||:::|||||:::|||||:::|||||
929 GTCCAAAGTGGACCTGGACAGGCTCAATGATGATGATCAAGCGTTACAGTT 978

34 yThrProArgAsnTyrSerValAsnLeuArgGluGluLeuLysLeuAla 50
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979 GCATCTCCAGGAATCACTCTGTGAACCTCAGGAGAGCTGAAGCTGACC 1028

51 AsnValValPhePheProArgCysLeuValGlnArgCysGlyGlyAs 67
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1029 ANTGCAGTCTTCTCCACAGATGCTCTCTGTGACGCGCTGTGTGGCNA 1078

67 nCysGlyCysGlyThrValAsnTrpArgSerCysThrCysAsnSerGlyL 84
|||||:::|||||:::|||||:::|||||:::|||||:::|||||
1079 CTGTGTTGGCGAACTGTCAACTGGAAGTCTGCACATGCAGCTCAGGGA 1128

84 yThrValLysLysTyrHisGluValLeuGlnPheGluProGlyHisLe 100
|||||:::|||||:::|||||:::|||||:::|||||:::|||||
1129 AGACAGTGAAGAAGTATCACAGAGTATTGAAGTTGAGCCTGGACATTC 1178

101 LysArgArgGlyArgAlaLysThrMetAlaLeuValAspLeuGlnLeu 117
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1179 AAGAGAGGGGCAAGCTAGAAATATGCCCTCTTGTGATATCCAGCTGGA 1228

117 pHISHisGluArgCysAspCysIleCysSerSerArgProProArg 132
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1229 TCATCATGAGCGATGTGACTGTATCTGACGCTCAAGACCACCTCGA 1274

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seq_name: /SIDS1/gcgdata/geneseq/geneseq/NA2000.DAT:AA81556

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AC  AA81556;
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DT  09-MAR-2001 (first entry)
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DE  Human growth factor homologue zveg4 degenerate DNA, SEQ ID NO:6.
XX
KW  Human; zveg4; growth factor homologue; VEGF/PDGF family;
KW  CUB domain; PDGF-like activity; mitogenic; osteogenic;
KW  neovascularisation; tissue repair; proliferation; differentiation;
KW  liver damage; neurodegenerative; Alzheimer's disease; multiple sclerosis;

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40 ervalAsnIleArgGluGluLeu...LysLeuAlaAsnValValPhePhe 55
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444  GCGTAGAAGTCGCCAGTCAGCTGGGAAGACAACAACACATCTTCTCAAG 493
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56  ProArgCysLeuValGlnArgCysGlyGlyAsnCysGlyCysGlyTh 72
   |||  |||:::  |||  |||  |||  |||  |||
494  CCCCCCTGTGTAATGCTCTCCGGTGTGGAGGCTGCTGC..... 532
   |||  |||  |||  |||  |||  |||  |||
72  rValAsnTrpArgSerCysThrCysAsnSerGlyLysThr.....V 86
   |||  |||  |||  |||  |||  |||  |||
533  ....AACGAAGAGGTGTGTGTATGACACACAGCACCTCTACATCT 578
   |||:::  ::|||  |||  ::|||  |||
86  allYsLysTyrHisGluVal.....LeuGlnPheGluProGlyHis 99
   |||:::  ::|||  |||  ::|||  |||
579  CCAACAGCTCTTTGAGATATCAGTCGCTGACATCAGTCCCC..... 622
   |||:::  ::|||  |||  ::|||  |||
100  IleLysArgArgGlyArgAlaLysThrMetAlaLeuValAspIleGlnLe 116
   |||:::  ::|||  |||  ::|||  |||
623  ....GAGTTAGTGCCTGTTAAAT 642
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seq_name: /cgn2_6/ptodata/2/lna/6B_COMB.seq:US-08-915-795-6

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seq documentation_block:
; Sequence 6, Application US/08915795
; Patent No. 6235713
; GENERAL INFORMATION:
; APPLICANT: Marc G. ACHEN
; APPLICANT: Andrew F. WILKS
; APPLICANT: Steven A. STACKER
; APPLICANT: Kari ALITALO
; TITLE OF INVENTION: GROWTH FACTOR
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Evenson, McKeown, Edwards & Lenahan P.L.L.C.
; STREET: 1200 G Street, NW, Suite 700
; CITY: Washington
; STATE: DC
; COUNTRY: United States of America
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/915,795
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: EVANS, Joseph D.
; REGISTRATION NUMBER: 26,269
; REFERENCE/DOCKET NUMBER: 1064/42983
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-8800
; TELEFAX: (202) 628-8844
; TELEX: N/A
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1325 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; TISSUE TYPE: Mouse Lung
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alignment_scores:
  Quality: 103.00      Length: 126
  Ratio: 1.661        Gaps: 6
  Percent Similarity: 49.206  Percent Identity: 26.984

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US-09-662-783-4 x US-08-915-795-6 ..
Align seg 1/1 to: US-08-915-795-6 from: 1 to: 1325

7  ArgTyrArgGlyArgSerTyrHisAspArgLysSerLysValAspLeuAs 23
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358  AGATTTCGGCAACTTTCTATGACACTGAAACACTAAAGTT..... 399
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23  parLeuAsnAspAspAlaLysArgTyrSerCysThrProArgAsnTyrS 40
   |||:::  ::|||  |||  ::|||  |||
400  ....ATAGATGAAGAATGGCAGAGGACCCCAATGACGCCCTAGAGACAT 445
   |||:::  ::|||  |||  ::|||  |||
40  ervalAsnIleArgGluGluLeu...LysLeuAlaAsnValValPhePhe 55
   |||:::  ::|||  |||  ::|||  |||
446  GCGTAGAAGTCGCCAGTCAGCTGGGAAGACAACAACACATCTTCTCAAG 495
   |||:::  ::|||  |||  ::|||  |||
56  ProArgCysLeuValGlnArgCysGlyGlyAsnCysGlyCysGlyTh 72
   |||  |||:::  |||  |||  |||  |||
496  CCCCCCTGTGTAATGCTCTCCGGTGTGGAGGCTGCTGC..... 534
   |||  |||  |||  |||  |||  |||
72  rValAsnTrpArgSerCysThrCysAsnSerGlyLysThr.....V 86
   |||  |||  |||  |||  |||  |||
535  ....AACGAAGAGGTGTGTGTATGACACACAGCACCTCTACATCT 580
   |||:::  ::|||  |||  ::|||  |||
86  allYsLysTyrHisGluVal.....LeuGlnPheGluProGlyHis 99
   |||:::  ::|||  |||  ::|||  |||
581  CCAACAGCTCTTTGAGATATCAGTCGCTGACATCAGTCCCC..... 624
   |||:::  ::|||  |||  ::|||  |||
100  IleLysArgArgGlyArgAlaLysThrMetAlaLeuValAspIleGlnLe 116
   |||:::  ::|||  |||  ::|||  |||
625  ....GAGTTAGTGCCTGTTAAAT 644

116  uAspHisHisGluArgCysAspCysIle 125
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645  TGCCAACCATACGGGTGTGTAAGTGTG 672

seq_name: /cgn2_6/ptodata/2/lna/6B_COMB.seq:US-08-915-795-4

seq documentation_block:
; Sequence 4, Application US/08915795
; Patent No. 6235713
; GENERAL INFORMATION:
; APPLICANT: Marc G. ACHEN
; APPLICANT: Andrew F. WILKS
; APPLICANT: Steven A. STACKER
; APPLICANT: Kari ALITALO
; TITLE OF INVENTION: GROWTH FACTOR
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Evenson, McKeown, Edwards & Lenahan P.L.L.C.
; STREET: 1200 G Street, NW, Suite 700
; CITY: Washington
; STATE: DC
; COUNTRY: United States of America
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/915,795
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: EVANS, Joseph D.
; REGISTRATION NUMBER: 26,269
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230 AGCGTGTGGT.....GGCTGCTCCCTCAGCATGGCGCTGAATGT 270
79 ThrCysAsnSerGlyLysThrValLysLysTyrHisGluValLeuGlnPh 95
   :::::  |||:::  :::::  |||:::
271 GTGCCACTGGGCAACACCAAGTCCGAATCCAGATCCTCATGATCCAGTA 320
95 eGluProGlyHisIleLysArgArgGlyArgAlaLysThrMetAlaLeu 112
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321 C.....CCGAGCAGTCAGCTGG 337
112 alaSpIleGlnLeuAspHisHisGluArgCysAspCysIleCysSerSer 128
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338 GGGAGATGTCCTGGGAAGACACAGCCCAATGTGAATGC..... 375
129 ArgProProArg 132
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376 AGACCAAAAAAA 387

seq_name: /cgn2_6/ptodata/2/ina/5B_COMB.seq:US-08-609-443B-8

seq_documentation_block:
; Sequence 8, Application US/08609443B
; Patent No. 5840693
; GENERAL INFORMATION:
; APPLICANT: ERIKSSON, Ulf
; APPLICANT: OLOFSSON, Birgitta
; APPLICANT: ALITALO, Kari
; APPLICANT: PAJUSOLA, Katri
; TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR-B AND
; TITLE OF INVENTION: DNA CODING THEREFOR
; NUMBER OF SEQUENCES: 57
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Evenson, McKeown, Edwards & Lenahan, P.L.L.C.
; STREET: 1200 G Street, N.W., Suite 700
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/609,443B
; FILING DATE: 01-MAR-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/397,651
; FILING DATE: 01-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/469,427
; FILING DATE: 06-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/569,063
; FILING DATE: 06-DEC-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: EVANS, Joseph D
; REGISTRATION NUMBER: 26,269
; REFERENCE/DOCKET NUMBER: 1064/41979CP4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-8800
; TELEFAX: (202) 628-8844
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 405 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; PS-08-609-443B-8

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  Quality: 95.50      Length: 104
  Ratio: 1.736       Gaps: 5
  Percent Similarity: 52.885      Percent Identity: 27.885

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  Align seg 1/1 to: US-08-609-443B-8 from: 1 to: 405

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133 CGTGCACATGCCAGCCAGGAGGTGGTGGCTCTGAGCATGGAAT 182
47 utylsLeuAlaAsnVal.....PhePheProArgCysLeuLeuValG 62
| : : : : : : : : : : : : : : : : : : : : : : : : :
183 C...ATGGCAATGGTCAACACACTAGTCCAGCTGTGTGACTGTGC 229
62 InArgCysGlyAsnCysGlyCysGlyThrValAsnTrpArgSerCys 78
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230 AGCGCTGTGGT.....GGCTGCTGCCCTGACGATGGCCTGGAATGT 270
79 ThrCysAsnSerGlyLysThrValLysLysTyrHisGluValLeuGlnPh 95
||||| :||||| :||||| :||| :||| :||| :||| :||| :|||
271 GTGCCACTGGGCACACCAAGTCCGATGCAGATCCTCATGATCCAGTA 320
95 eGluProGlyHisIleLysArgArgGlyArgAlaLysThrMetAlaLeuV 112
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321 C.....CCGACGACGTGACGTGG 337
112 alaSpIleGlnLeuAspHisHisGluArgCysAspCysLeuSerSer 128
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338 GGGAGATGTCCTGGGAAGAACACAGCAATGTGAATGC..... 375
129 ArgProProArg 132
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376 AGACCAAAAAA 387

seq_name: /cgn2_6/ptodata/2/ina/5B_COMB.seq:US-08-569-063C-8

seq_documentation_block:
; Sequence 8, Application US/08569063C
; Patent No. 5928939
; GENERAL INFORMATION:
; APPLICANT: ERIKSSON, Ulf
; APPLICANT: OLOFSSON, Birgitta
; APPLICANT: ALITALO, Kari
; APPLICANT: PAJUSOLA, Katri
; TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR-B AND
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Evenson, McKeown, Edwards & Lenahan, P.L.L.C.
; STREET: 1200 G Street, N.W., Suite 700
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/569,063C
; FILING DATE: 06-DEC-1995
; PRIOR APPLICATION NUMBER: US 08/469,427
; FILING DATE: 06-JUN-1995
; PRIOR APPLICATION NUMBER: US 08/397,651
; FILING DATE: 01-MAR-1995
; ATTORNEY/AGENT INFORMATION:

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; NAME: EVANS, Joseph D
; REGISTRATION NUMBER: 26,269
; REFERENCE/DOCKET NUMBER: 1064/41979CP3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-8800
; TELEFAX: (202) 628-8844
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 405 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; US-08-569-063C-8

alignment_scores:
  Quality: 95.50      Length: 104
  Ratio: 1.736       Gaps: 5
  Percent Similarity: 52.885      Percent Identity: 27.885

alignment_block:
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  Align seg 1/1 to: US-08-569-063C-8 from: 1 to: 405

31 ArgTyrSerCysThrProArgAsnTyrSerValAsnIleArgGluGluLeu 47
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133 CGTGCACATGCCAGCCAGGAGGTGGTGGCTCTGAGCATGGAAT 182
47 utylsLeuAlaAsnVal.....PhePheProArgCysLeuLeuValG 62
| : : : : : : : : : : : : : : : : : : : : : : : : :
183 C...ATGGCAATGGTCAACACACTAGTCCAGCTGTGTGACTGTGC 229
62 InArgCysGlyAsnCysGlyCysGlyThrValAsnTrpArgSerCys 78
||||| :||||| :||||| :||| :||| :||| :||| :||| :|||
230 AGCGCTGTGGT.....GGCTGCTGCCCTGACGATGGCCTGGAATGT 270
79 ThrCysAsnSerGlyLysThrValLysLysTyrHisGluValLeuGlnPh 95
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271 GTGCCACTGGGCACACCAAGTCCGATGCAGATCCTCATGATCCAGTA 320
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321 C.....CCGACGACGTGACGTGG 337
112 alaSpIleGlnLeuAspHisHisGluArgCysAspCysLeuSerSer 128
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338 GGGAGATGTCCTGGGAAGAACACAGCAATGTGAATGC..... 375
129 ArgProProArg 132
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376 AGACCAAAAAA 387

seq_name: /cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-469-427A-4

seq_documentation_block:
; Sequence 4, Application US/08469427A
; Patent No. 5607918
; GENERAL INFORMATION:
; APPLICANT: ERIKSSON, Ulf
; APPLICANT: OLOFSSON, Birgitta
; APPLICANT: ALITALO, Kari
; APPLICANT: PAJUSOLA, Katri
; TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR-B AND
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Evenson, McKeown, Edwards & Lenahan
; STREET: 1200 G Street, N.W., Suite 700
; CITY: Washington
; STATE: DC
; ZIP: 20005

```



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62 lnArgCysGlyAsnCysGlyCysGlyThrValAsnTrpArgSerCys 78
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225 AGCGCTGTGGT.....GGCTGCTGCCCTGACGATGGCTGGAATGT 265
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79 ThrCysAsnSerGlyThrValLysLysTyrHisGluValLeuGlnPh 95
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
266 GTGCCCACTGGCCACCAACCAAGTCGAATGCATCCATCATCCAGTA 315
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
95 eGluProGlyHisIleLysArgGlyArgAlaLysThrMetAlaLeuV 112
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316 C.....CGGACGCTCAGCTGG 332
112 alAspIleGlnLeuAspHisGluArgCysAspCysSerser 128
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333 GGGAGATGCTCCCTGGGAAGAACACAGCAATGTGAATGC..... 370
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seq_name: /cgn2_6/ptodata/2/ina/5B_COMB.seq:US-08-569-063C-4

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seq_documentation_block:
; Sequence 4, Application US/08569063C
; Patent No. 5928939
; GENERAL INFORMATION:
; APPLICANT: ERIKSSON, Ulf
; APPLICANT: OLOFSSON, Birgitta
; APPLICANT: ALITALO, Kari
; APPLICANT: PAJUSOLA, Katri
; TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR-B AND
; TITLE OF INVENTION: DNA CODING THEREFOR
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Evenson, McKeown, Edwards & Lenahan, P.L.L.C.
; STREET: 1200 G Street, N.W., Suite 700
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/569,063C
; FILING DATE: 06-DEC-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/469,427
; FILING DATE: 06-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/397,651
; FILING DATE: 01-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: EVANS, Joseph D
; REGISTRATION NUMBER: 26,269
; REFERENCE/DOCKET NUMBER: 1064/41979CP3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-8800
; TELEFAX: (202) 628-8844
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 565 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; TISSUE TYPE: adult mouse heart
; US-08-569-063C-4

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alignment_scores:
  Quality: 95.50      Length: 104
  Ratio: 1.736      Gaps: 5
  Percent Similarity: 52.885      Percent Identity: 27.885

alignment_block:
US-09-662-783-4 x US-08-569-063C-4 ..
Align seg 1/1 to: US-08-569-063C-4 from: 1 to: 565

31 ArgTyrSerCysThrProArgAsnTyrSerValAsnIleArgGluGluLe 47
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
128 CGTGCACATGCCAGCCAGGAGGTGGTGGCTCTGAGCATGGAACT 177
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
47 ulysLeuAlaAsnValVal.....PhePheProArgCysLeuLeuValG 62
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
178 C...ATGGCAATGGTCAAAACAACTAGTCCCACTGTGTGACTGTGC 224
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
62 lnArgCysGlyGlyAsnCysGlyCysGlyThrValAsnTrpArgSerCys 78
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
225 AGCGCTGTGGT.....GGCTGCTGCCCTGACGATGGCTGGAATGT 265
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
79 ThrCysAsnSerGlyThrValLysLysTyrHisGluValLeuGlnPh 95
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
266 GTGCCCACTGGCCACCAACCAAGTCGAATGCATCCATCATCCAGTA 315
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
95 eGluProGlyHisIleLysArgGlyArgAlaLysThrMetAlaLeuV 112
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
316 C.....CGGACGCTCAGCTGG 332
112 alAspIleGlnLeuAspHisGluArgCysAspCysSerser 128
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
333 GGGAGATGCTCCCTGGGAAGAACACAGCAATGTGAATGC..... 370
129 ArgProProArg 132
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371 AGACCAAAAAA 382

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seq_name: /cgn2_6/ptodata/2/ina/5B_COMB.seq:US-08-609-443B-12

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seq_documentation_block:
; Sequence 12, Application US/08609443B
; Patent No. 5840693
; GENERAL INFORMATION:
; APPLICANT: ERIKSSON, Ulf
; APPLICANT: OLOFSSON, Birgitta
; APPLICANT: ALITALO, Kari
; APPLICANT: PAJUSOLA, Katri
; TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR-B AND
; TITLE OF INVENTION: DNA CODING THEREFOR
; NUMBER OF SEQUENCES: 57
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Evenson, McKeown, Edwards & Lenahan, P.L.L.C.
; STREET: 1200 G Street, N.W., Suite 700
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/609,443B
; FILING DATE: 01-MAR-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/397,651
; FILING DATE: 01-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/469,427

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;; FILING DATE: 06-JUN-1995
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/569,063
;; FILING DATE: 06-DEC-1995
;; ATTORNEY/AGENT INFORMATION:
;; NAME: EVANS, Joseph D
;; REGISTRATION NUMBER: 26,269
;; REFERENCE/DOCKET NUMBER: 1064/41979CP4
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (202) 628-8800
;; TELEFAX: (202) 628-8844
;; INFORMATION FOR SEQ ID NO: 12:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 624 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: cDNA
;; HYPOTHETICAL: NO
;; ORIGINAL SOURCE:
;; TISSUE TYPE: mouse
US-08-609-443B-12

alignment_scores:
Quality: 95.50 Length: 104
Ratio: 1.736 Gaps: 5
Percent Similarity: 52.885 Percent Identity: 27.885

alignment_block:
US-09-662-783-4 x US-08-609-443B-12 ..

Align seg 1/1 to: US-08-609-443B-12 from: 1 to: 624

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31 ArgTyrSerCysThrProArgAsnTyrSerValAsnIleArgGluGluLeu 47
130 CGTGGCAATGCCAGCCAGGAGGTGGTGGCTCTGTGAGCTGGAAT 179
47 uLysLeuAlaAsnValVal.....PhePheProArgCysLeuLeuValG 62
180 C...ATGGCAATGGTGTCAACAACACTAGTCCAGCTGTGTGACTGTGC 226
62 lnArgCysGlyGlyAsnCysGlyThrValAsnTrpArgSerCys 78
227 AGCGCTGTGGT.....GGCTGCTGCCCTGACGATGGCTGGAATGT 267
79 ThrCysAsnSerGlyLysThrValLysLysTyrHisGluValLeuGlnPh 95
268 GTGCCCCAGTGGGCAACCAAGTCCGAATGCAGATCCTCATGATCCAGTA 317
95 eGluProGlyHisIleLysArgArgGlyArgAlaLysThrMetAlaLeuV 112
318 C.....CCGAGCAGTCAGCTGG 334
112 alaSpIleGlnLeuAspHisHisGluArgCysAspCysIleCysSerSer 128
335 GGGAGATGTCTCTGGAGAACACACACCAATGTGAATGC..... 372
129 ArgProProArg 132
373 AGACCAAAAAAA 384
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seq_name: /cgn2_6/ptodata/2/ina/5B_comb.seq:US-08-569-063C-12

seq_documentation_block:

;; Sequence 12, Application US/08569063C
;; Patent No. 5928939
;; GENERAL INFORMATION:
;; APPLICANT: ERIKSSON, Ulf
;; APPLICANT: OLOFSSON, Birgitta
;; APPLICANT: ALITALO, Kari
;; APPLICANT: PAJUSOLA, Katri
;; TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR-B AND

;; TITLE OF INVENTION: DNA CODING THEREFOR
;; NUMBER OF SEQUENCES: 23
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Evenson, McKeown, Edwards & Lenahan, P.L.L.C.
;; STREET: 1200 G Street, N.W., Suite 700
;; CITY: Washington
;; STATE: DC
;; COUNTRY: USA
;; ZIP: 20005
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/569,063C
;; FILING DATE: 06-DEC-1995
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/469,427
;; FILING DATE: 06-JUN-1995
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/397,651
;; FILING DATE: 01-MAR-1995
;; ATTORNEY/AGENT INFORMATION:
;; NAME: EVANS, Joseph D
;; REGISTRATION NUMBER: 26,269
;; REFERENCE/DOCKET NUMBER: 1064/41979CP3
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (202) 628-8800
;; TELEFAX: (202) 628-8844
;; INFORMATION FOR SEQ ID NO: 12:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 624 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: cDNA
;; HYPOTHETICAL: NO
;; ORIGINAL SOURCE:
;; TISSUE TYPE: mouse
US-08-569-063C-12

alignment_scores:
Quality: 95.50 Length: 104
Ratio: 1.736 Gaps: 5
Percent Similarity: 52.885 Percent Identity: 27.885

alignment_block:

US-09-662-783-4 x US-08-569-063C-12 ..

Align seg 1/1 to: US-08-569-063C-12 from: 1 to: 624

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31 ArgTyrSerCysThrProArgAsnTyrSerValAsnIleArgGluGluLeu 47
130 CGTGGCAATGCCAGCCAGGAGGTGGTGGCTCTGTGAGCTGGAAT 179
47 uLysLeuAlaAsnValVal.....PhePheProArgCysLeuLeuValG 62
180 C...ATGGCAATGGTGTCAACAACACTAGTCCAGCTGTGTGACTGTGC 226
62 lnArgCysGlyGlyAsnCysGlyThrValAsnTrpArgSerCys 78
227 AGCGCTGTGGT.....GGCTGCTGCCCTGACGATGGCTGGAATGT 267
79 ThrCysAsnSerGlyLysThrValLysLysTyrHisGluValLeuGlnPh 95
268 GTGCCCCAGTGGGCAACCAAGTCCGAATGCAGATCCTCATGATCCAGTA 317
95 eGluProGlyHisIleLysArgArgGlyArgAlaLysThrMetAlaLeuV 112
318 C.....CCGAGCAGTCAGCTGG 334
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39 CQTGCCACATGCGACGCCAGGAGGTGGTGCCCTCTGAGCATGGAAC 88
47 uLysLeuLaAsnValVal.....PhePheProArgCysLeuLeuValG 62
89 C...ATGGCAATCTGGTCAACAACATAGTGCACAGCTGTGTGACCTGC 135
62 InArACvsgLgLVasnCvsgLgVCvsgLgVthrValAsnTrpArqSerCys 78

136 AGCGCTGTGGT.....GGCTGCTGCCCTGACGATGGCCCTGGAATGT 176

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79 ThrCysAsnSerGlyLysThrValLysLysTyrrHisGluValLeuGlnPh 95
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177 GTGCCCATGGGACACCAAGTCCGGAATGCAGATCCTCATGTATCCAGTA 226
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95 eGluProGlyHisIleLysArgGlyArgAlaLysThrMetAlaLeu 112
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227 C.....CCGAGTCAGTCCTGG 243
      : : : : : : : : : : : : : : : : : : : : : : : : : : :
112 alaspIeclneuspHisGluArgCysAspCysIleCysSerSer 128
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129 ArgProProArg 132
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282 AGACCAAAAAAA 293

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Documentation block:
 Reference 1, Application US/08609443B
 Patent No. 5840693
 GENERAL INFORMATION:
 APPLICANT: ERIKSSON, Ulf
 APPLICANT: OLOFSSON, Birgitta
 APPLICANT: ALITALO, Kari

APPLICANT: PAJUSOLA, Katri
TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR-B
TITLE OF INVENTION: DNA CODING THEREFOR
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:

ADDRESSEE: Evenson, McKeown, Edwards & Lenahan, P.L.L.C.
STREET: 1200 G Street, N.W., Suite 700
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/609,443B
FILING DATE: 01-MAR-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/397,651
FILING DATE: 01-MAR-1995
PRIOR APPLICATION DATA:

FILING DATE: 06-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/569,063
FILING DATE: 06-DEC-1995
ATTORNEY/AGENT INFORMATION:

NAME: EVANS, JOSEPH D
REGISTRATION NUMBER: 26,269
REFERENCE/DOCKET NUMBER: 1064/41979CP4
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-8800
TELEFAX: (202) 628-8844
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:

TELEFAX: (202) 626-6644
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:

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; LENGTH: 886 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; TISSUE TYPE: mouse embryo
; IMMEDIATE SOURCE:
; CLONE: pcif2
; US-08-609-443B-1

alignment_scores:
    Quality: 95.50      Length: 104
    Ratio: 1.736       Gaps: 5
    Percent Similarity: 52.885    Percent Identity: 27.885

alignment_block:
US-09-662-783-4 x US-08-609-443B-1 ..
Align seg 1/1 to: US-08-609-443B-1 from: 1 to: 886

31 ArgTyrSerCysThrProArgAsnTyrSerValAsnIleArgGluGluLe 47
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39 CGTGCCACATGCCAGCCAGGAGGTGGTGGCTCTGAGCATGGAAGT 88
;
47 uLysLeuAlaAsnValVal.....PhePheProArgCysLeuLeuValG 62
| :||| :||| :||| :||| :||| :||| :||| :||| :|||
89 C...ATGGCAATGTGTCAACCAACTAGTGCACGCTGTGTGACTGTGC 135
;
62 InArgCysGlyGlyAsnCysGlyCysGlyThrValAsnTyrArgSerCys 78
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136 AGCGCTGTGT.....GGCTGCTGCCCTGACGATGCCCTGGAATGT 176
;
79 ThrCysAsnSerGlyLysThrValLysLysTyrHisGluValLeuGlnPh 95
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177 GTGCCACATGGGCAACCAAGTCCGAATGCAGATCCTCATGATCCAGTA 226
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95 eGluProGlyHisIleLysArgArgGlyArgAlaLysThrMetAlaLeuV 112
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227 C.....CCGAGCAGTCAGCTGG 243
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112 alaSpIleGlnLeuAspHisHisGluArgCysAspCysIleCysSerSer 128
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244 GGGAGATGTCCCTGGAAGAACACAGCCAAATGTGAATGC.....281

129 ArgProProArg 132
||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
282 AGACCAAAAAA 293

seq_name: /cgn2_6/ptodata/2/ina/5B_COMB.seq:US-08-569-063C-1

seq_documentation_block:
; Sequence 1, Application US/08569063C
; Patent No. 5928939
; GENERAL INFORMATION:
; APPLICANT: ERIKSSON, Ulf
; APPLICANT: OLOFSSON, Birgitta
; APPLICANT: ALITALO, Kari
; APPLICANT: PAJUSOLA, Katri
; TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR-B AND
; TITLE OF INVENTION: DNA CODING THEREFOR
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Evenson, McKeown, Edwards & Lenahan, P.L.L.C.
; STREET: 1200 G Street, N.W., Suite 700
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

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Result No.	Score	Query		Length	DB	ID	Description
		Match	%				
1	737	100.0		370	4	Q9GZP0	Q9GZP0 homo sapien
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3	338.5	45.9		345	13	Q91946	Q91946 gallus gall
4	328.5	44.6		345	4	Q9UL22	Q9UL22 homo sapien
5	328.5	44.6		345	4	Q9NRA1	Q9NRA1 homo sapien
6	324.5	44.0		345	11	Q9QX71	Q9QX71 mus musculus
7	322.5	43.8		345	11	Q9EQX6	Q9EQX6 rattus norv
8	316.5	42.9		345	11	Q9JHV8	Q9JHV8 mus musculus
9	107	14.5		326	11	Q35251	Q35251 rattus norv
10	103	14.0		354	4	Q43915	Q43915 homo sapien
11	103	14.0		358	11	P97946	P97946 mus musculus
12	97.5	13.2		150	11	O54881	O54881 rattus norv
13	97	13.2		304	5	Q9N413	Q9N413 caenorhabdi
14	95.5	13.0		207	11	O64290	O64290 mus musculus
15	89	12.1		418	13	O57352	O57352 coturnix co
16	88.5	12.0		301	5	Q9WP65	Q9WP65 drosophila
17	88	11.9		149	11	Q9WVQ7	Q9WVQ7 mesocricetu
18	87.5	11.9		195	13	Q9DE50	Q9DE50 brachydania
19	87	11.8		420	6	O9XS50	O9XS50 bos taurus

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Db 299 VORCGNCGGTNNRSCNCGTKVKKYHEVLQFEPGHIKRRGRKTMALVDIQLDHE 358
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Db 359 RDCICSSRRPR 370
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RESULT 2
Q9EQT1 PRELIMINARY; PRT; 370 AA.
AC Q9EQT1;
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DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE SPINAL-CORD DERIVED GROWTH FACTOR-B.
GN RSCDGF-B.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA Hamada T., Ui-Tei K., Inaki J., Miyata Y.;
RT "Molecular Cloning of SCDF-B, a Novel Growth Factor Homologous to
RT SCDFG/PDGF-C/falotein.";
RL Biochem. Biophys. Res. Commun. 0:0-0(2000).
DR EMBL; AB052170; BAB18920.1; -.
SQ SEQUENCE 370 AA; 42809 MW; 7B8A251F679BF73 CRC64;

Query Match 92.5%; Score 682; DB 11; Length 370;
Best Local Similarity 88.6%; Pred. No. 4.8e-68;
Matches 117; Conservative 10; Mismatches 5; Indels 0; Gaps 0;

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Db 299 VORCGNCGGTNNRSCNCGTKVKKYHEVLQFEPGHIKRRGRKTMALVDIQLDHE 358
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QY 121 RDCICSSRRPR 132
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RESULT 3
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AC Q91946;
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DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE SPINAL-CORD-DERIVED GROWTH FACTOR.
GN Gallus gallus (Chicken).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN-WHITE LEGHORN; TISSUE=SPINAL CORD;
RX MEDLINE=20317014; PubMed=10858496;
RA Hamada T., Ui-Tei K., Miyata Y.;
RT "A novel gene derived from developing spinal cords, SCDF, is a unique
RT member of the PDGF/VEGF family.";
RL FEBS Lett. 475:97-102(2000).
DR EMBL; AB033829; BAB03265.1; -.
DR InterPro; IPR000859; -.
DR Pfam; PF00431; CUB; 1.
DR PROSITE; PS01180; CUB; 1.
DR PROSITE; PS0278; PDGF_2; 1.
DR SMART; SM00042; CUB; 1.
SQ SEQUENCE 345 AA; 39029 MW; CDE9E51F40633E78 CRC64;

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Best Local Similarity 49.2%; Pred. No. 1.2e-28;
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QY 1 MYLDTPRYGRSYHDRKSKVDLRLNDDAKRYSCTPRNYSVNIREELKLANVFFPR 58
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QY 59 LLVQRCGGNCGGTNNRSCNCGTKVKKYHEVLQFEPGHIKRRGRKTMALVDIQLD 118
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DR PROSITE; PS01180; CUB; 1.
DR PROSITE; PS0278; PDGF_2; 1.
DR SMART; SM00042; CUB; 1.
SQ SEQUENCE 345 AA; 38940 MW; 97ACEA992BF5128C CRC64;

Query Match 45.9%; Score 338.5; DB 13; Length 345;
Best Local Similarity 50.4%; Pred. No. 8.9e-30;
Matches 65; Conservative 21; Mismatches 36; Indels 7; Gaps 4;

QY 1 MYLDTPRYGRSYHDRKSKVDLRLNDDAKRYSCTPRNYSVNIREELKLANVFFPR 58
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QY 59 LLVQRCGGNCGGTNNRSCNCGTKVKKYHEVLQFEPGHIKRRG-RAKTMALVDIQLD 117
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QY 118 HHERCDIC 126
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Db 331 HHEECDCVC 339
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RESULT 4
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AC Q9UL22;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
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DE GROWTH FACTOR).
GN HSCDGF.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=UTERUS;
RA Tsai Y.J., Lee R.K.K., Lin S.P.;
RT "Fallotein, a novel growth factor like gene identified in human
RT uterus.";
RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=BRIN;
RX MEDLINE=20317014; PubMed=10858496;
RA Hamada T., Ui-Tei K., Miyata Y.;
RT "A novel gene derived from developing spinal cords, SCDF, is a unique
RT member of the PDGF/VEGF family.";
RL FEBS Lett. 475:97-102(2000).
DR EMBL; AF091434; AAF00049.1; -.
DR EMBL; AB033831; BAB03266.1; -.
DR InterPro; IPR000072; -.
DR InterPro; IPR000859; -.
DR Pfam; PF00341; PDGF; 1.
DR Pfam; PF00431; CUB; 1.
DR PROSITE; PS01180; CUB; 1.
DR PROSITE; PS0278; PDGF_2; 1.
DR SMART; SM00042; CUB; 1.
SQ SEQUENCE 345 AA; 39029 MW; CDE9E51F40633E78 CRC64;

Query Match 44.6%; Score 328.5; DB 4; Length 345;
Best Local Similarity 49.2%; Pred. No. 1.2e-28;
Matches 63; Conservative 20; Mismatches 40; Indels 5; Gaps 3;

QY 1 MYLDTPRYGRSYHDRKSKVDLRLNDDAKRYSCTPRNYSVNIREELKLANVFFPR 58
    :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 215 LYRPTWLLGKAYFGRKSRVVDLRLNLTTEVRLYSTPRNFVSIREELKRTDTIWPGL 274
    :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 59 LLVQRCGGNCGGTNNRSCNCGTKVKKYHEVLQFEPGHIKRRGRKTMALVDIQLD 118
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

```


RESULT	6
Q90Y71	
ID	PRELIMINARY;
AC	Q90Y71; PRT; 345 AA.
DT	01-MAY-2000 (TREMBLrel. 13, Created)
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT	01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE	FALLOTEIN.
OS	Mus musculus (Mouse).
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX	NCB1_TaxID=10090;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	TISSUE=OVARY;
RA	Tsai Y.-J., Lee R.K.-K., Chen Y.-H., Lin S.-P., Cheng W.T.-K.;

Q9JHV8
ID Q9JHV8 PRELIMINARY; PRT: 345 AA.

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SQ SEQUENCE 326 AA; 37112 MW; 1261AFA373596C00 CRC64;

Query Match 14.5%; Score 107; DB 11; Length 326;
Best Local Similarity 27.8%; Pred.No. 0.00055;
Matches 35; Conservative 17; Mismatches 46; Indels 28; Gaps

QY 7 RYRGRSYHDKRSKYDLDRLNDADAKRYSCPTPNYSVNIRBEL-KLANVWFFPRCLLVORCG 65
   I: I: I: I: I: I: I: I: I: I: I: I: I: I: I: I: I: I: I: I: I: I:
Db 93 RFAATFYDTETLKV-----IDEWQRTQCSPRETCVEASELGKTTTFFKPPCVNVFRCG 148
   I: I: I: I: I: I: I: I: I: I: I: I: I: I: I: I: I: I: I: I: I: I:

QY 66 GNCGGCTVNNRSTCSNGKT---VKYHEV---LQEPGHIKRRGRAKTMALVDIQLDHH 119
   I: I: I: I: I: I: I: I: I: I: I: I: I: I: I: I: I: I: I: I: I: I:
Db 149 GCC-----NEESVMCMNTSTSYISKQLFEISVPLTSVP-----ELVPVKIANH 191
   I: I: I: I: I: I: I: I: I: I: I: I: I: I: I: I: I: I: I: I: I: I:

QY 120 ERCDCI 125
   I: I:
Db 192 TGCKCL 197

RESULT 10
O43915 PRELIMINARY; PRT; 354 AA.
ID O43915
AC O43915;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE GROWTH FACTOR FIGF.
FE FIGF OR VEGF-D.
GS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP MEDLINE FROM N.A.
RX MEDLINE=981140120; PubMed=9479493;
RA Rocchigiani M., Lestingi M., Luddi A., Orlandini M., Franco B.,
RA Rossi E., Ballabio A., Zuffardi O., Oliviero S.;
RT "Human FIGF: cloning, gene structure, and mapping to chromosome xp22.1
RT between the FIGA and the GRPR genes.";
RL Genomics 47:207-216(1998).
[2]
RP SEQUENCE FROM N.A.
RX TISSUE=LUNG;
RA MEDLINE=97349118; PubMed=9205122;
RA Yamada Y., Nezu J., Shimane M., Hirata Y.;
RT "Molecular cloning of a novel vascular endothelial growth factor,
RT VEGF-D.";
RL Genomics 42:483-488(1997).
[3]
RP SEQUENCE FROM N.A.
RX MEDLINE=98118549; PubMed=9435229;
RA Achen M.G., Jeltsch M., Kukk E., Maekinen T., Vitali A., Wilks A.F.,
RA Alitalo K., Stacker S.A.;
RT "Vascular endothelial growth factor D (VEGF-D) is a ligand for the
RT tyrosine kinases VEGF receptor 2 (Flk1) and VEGF receptor 3 (Flt4).";
RL Proc. Natl. Acad. Sci. U.S.A. 95:548-553(1998).
DR EMBL; Y12864; CAA73371.1; JOINED.
DR EMBL; Y12865; CAA73371.1; JOINED.
DR EMBL; Y12866; CAA73371.1; JOINED.
DR EMBL; Y12867; CAA73371.1; JOINED.
DR EMBL; Y12868; CAA73371.1; JOINED.
DR EMBL; Y12869; CAA73371.1; JOINED.
DR EMBL; Y12870; CAA73371.1; JOINED.
DR EMBL; D89630; BAA24264.1; -.
DR EMBL; AJ000185; CAA03942.1; -.
DR EMBL; Y12863; CAA73370.1; -.
DR HSSP; P15692; 1VPP.
DR InterPro; IPR000072; -.
DR Pfam; PF00341; PDGF; 1.
DR ProDom; PD001629; -; 1.
DR PROSITE; PS00249; PDGF_1; 1.
DR PROSITE; PS00278; PDGF_2; 1.

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DB	ID	Accession	Species	Length	Score	DB	Indels	Gaps
Db	149	GCC-----NEEGVMCMNTSTSYISKOLFEISVPLTSVP		150	AA.			
QY	120	ERCDCI 125						
Db	192	TCCKCL 197						
RESULT	12							
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ID	O54881	PRELIMINARY;	PRT;	150	AA.			
AC	O54881;							
DT	01-JUN-1998	(TrEMBLrel. 06, Created)						
DT	01-JUN-1998	(TrEMBLrel. 06, Last sequence update)						
DT	01-NAR-2001	(TrEMBLrel. 16, Last annotation update)						
DE	VASCULAR ENDOTHELIAL GROWTH FACTOR B (FRAGMENT).							
OS	Rattus norvegicus (Rat).							
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;							
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus							
NCBI	TaxID=10116;							
RN	[1]							
RP	SEQUENCE FROM N.A.							
RC	TISSUE=HEART;							
RL	Weil J., Eschenhagen T., Mittmann C., Scholz H.;							
RA	Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.							
DR	EMBL; AF022952; AAB95447.1;							
DR	HSSP; P15692; 1VPP.							
DR	InterPro: IPR000072;							
DR	Pfam: PF00341; PDGF_1;							
DR	PROSITE: PS00249; PDGF_1;							
DR	PROSITE: PS0278; PDGF_2;							
DR	SMART; SM00141; PDGF; 1.							
FT	NON_TER 1							
FT	NON_TER 150							
FT	SEQUENCE 150 AA; 17243 MW; E2AC5CA9AD942F6A CRC64;							
Query Match	13.28;	Score	97.5;	DB	11;	Length	150;	
Best Local Similarity	28.88;	Pred. No.	0.0029;					
Matches	30; Conservative	15; Mismatches	38; Indels	21; Gaps				
QY	31	RYSCPTPRNYSVNIIEUKLANV--FPFRCLLVORCGNGCGTVMNRSCTCNSGKTVKK 88						
Db	13	RATCQPREVVVPLSMFEF-MGNVVXQFVPSCVTVQRCG--GCCPDDGLECPVIGHQVRM 68						
QY	89	YHEVLQFEGHKRGRKTMALVDIOLDHHERCDCICSSRP 132						
Db	69	QILMIOY-----PSSQLGEMSLERHSQCE-----RPKR 97						
RESULT	13							
Q9N413								
ID	Q9N413	PRELIMINARY;	PRT;	304	AA.			
AC	Q9N413;							
DT	01-OCT-2000	(TrEMBLrel. 15, Created)						
DT	01-OCT-2000	(TrEMBLrel. 15, Last sequence update)						
DT	01-NAR-2001	(TrEMBLrel. 16, Last annotation update)						
DE	Y3A3CL.6 PROTEIN.							
GN	Y3A3CL.6.							
OC	Caenorhabditis elegans.							
OC	Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;							
OC	Rhabditidae; Peloderinae; Caenorhabditis.							
NCBI	TaxID=6239;							
RN	[1]							
RP	SEQUENCE FROM N.A.							
RC	STRAIN=BRISTOL N2;							
RA	MEDLINE=99069613; PubMed=9851916;							
RX	None;							
RT	"Genome sequence of the nematode C. elegans: a platform for							
RT	investigating biology. The C. elegans Sequencing Consortium."							
RL	Science 282:2012-2018(1998).							
RN	[2]							
RP	SEQUENCE FROM N.A.							

RC STRAIN-BRISTOL N2;
RA Waterston R.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC024763; AAF60517.1; -
DR InterPro; IPR000072; -
DR InterPro; IPR001839; -
DR PROSITE; PS0278; PDGF_2; 1.
DR PROSITE; PS00250; TGF_BETA; UNKNOWN_1.
DR SMART; SM00141; PDGF; 1.
SQ SEQUENCE 304 AA; 34131 MW; FB55120F513634D5 CRC64;

Query Match 13.2%; Score 97; DB 5; Length 304;
Best Local Similarity 26.9%; Pred. No. 0.0067;
Matches 32; Conservative 21; Mismatches 48; Indels 18; Gaps 6;

QY 17 KSKVDLRLNDADAKRYSCTPRNSVNIIEELKLANVVFPRCLLVORCGGCGGVNWR 76
DB 102 QSMKDKQGN-----TCNLQSVCPVPIQLSDPPQVLMYPKCYEVKOCVGC-CNSVE-- 153
QY 77 SCTNSG--KTVKKYHEVLQFEGPHIKRRGRAKTMALVDIQLDHERCDDCI-CSSRPPR 132
DB 154 --TCHPGTINLYKKHVAELLY-----IGNGRFNFMTKEITMEEHTSCSCFDCGSGNTPO 205

RESULT 14
Q64290 PRELIMINARY; PRT; 207 AA.
AC Q64290;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE VASCULAR ENDOTHELIAL GROWTH FACTOR RELATED PROTEIN (VASCULAR
DE ENDOTHELIAL GROWTH FACTOR B 186).
GN VEGFB OR VRF OR VEGF-B.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=HEART;
RX MEDLINE=96197355; PubMed=8637916;
RA Olofsson B.;
RT "Vascular endothelial growth factor B, a novel growth factor for
RT endothelial cells.";
RL Proc. Natl. Acad. Sci. U.S.A. 93:2576-2581(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=HEART;
RX MEDLINE=96325041; PubMed=8702615;
RA Olofsson B., Pajusola K., von Euler G., Chilov D., Alitalo K.,
RA Eriksson U.;
RT "Genomic organization of the mouse and human genes for vascular
RT endothelial growth factor B (VEGF-B) and characterization of a second
RT splice isoform.";
RL J. Biol. Chem. 271:19310-19317(1996).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=WHOLE BRAIN;
RX MEDLINE=96183052; PubMed=8607868;
RA Townson S., Lagercrantz J., Grimmond S., Silins G., Nordenskjold M.,
RA Weber G., Hayward N.K.;
RT "Characterization of the murine VEGF-related factor gene.";
RT Biochem. Biophys. Res. Commun. 220:922-928(1996).
DR EMBL; U52820; AAC52823.1; -
DR EMBL; U43836; AAC52932.1; -
DR HSP; PL5692; IVPP.
DR MGI; MGI:106199; Vegfb.
DR InterPro; IPR000072; -
DR Pfam; PF00341; PDGF; 1.
DR ProDom; PD001629; -; 1.
DR PROSITE; PS00249; PDGF_1; 1.

DR PROSITE; PS0278; PDGF_2; 1.
DR SMART; SM00141; PDGF; 1.
SQ SEQUENCE 207 AA; 21914 MW; 4817A5B96F6960C2 CRC64;

Query Match 13.0%; Score 95.5; DB 11; Length 207;
Best Local Similarity 27.9%; Pred. No. 0.0066;
Matches 29; Conservative 16; Mismatches 38; Indels 21; Gaps 5;

QY 31 RYSCTPRNSVNIIEELKLANVVFPRCLLVORCGGCGGVNWRSTCNSGKTGK 88
DB 44 RATCPQREVVVPLSMEL-MGNVVKQLVPSCVTVORCG--GCCPDDGLECVPTGQHOVRM 99
QY 89 YHEVLQFEGPHIKRRGRAKTMALVDIQLDHERCDDCISSRPPR 132
DB 100 QILMIQY-----PSSQLGEMSLSEHSQCEC-----RPAK 128

RESULT 15
O57352 PRELIMINARY; PRT; 418 AA.
AC O57352;
DT 01-JUN-1998 (TREMBLrel. 06, Created)
DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE VASCULAR ENDOTHELIAL GROWTH FACTOR C PRECURSOR.
GN VEGF-C.
OS Coturnix coturnix japonica (Japanese quail).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauaria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Coturnix.
OX NCBI_TaxID=93934;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98167900; PubMed=9435294;
RA Eichmann A., Corbel C., Jaifredo T., Breant V., Joukov V., Kumar V.,
RA Alitalo K., Le Douarin N.M.;
RT "Avian VEGF-C: cloning, embryonic expression pattern and stimulation
RT of the differentiation of VEGFR2-expressing endothelial cell
RT precursors.";
RL Development 125:743-752(1998).
DR EMBL; Y15837; CAA75799.1; -
DR HSP; PL5692; IVPP.
DR InterPro; IPR000072; -
DR InterPro; IPR002400; -
DR Pfam; PF00341; PDGF; 1.
DR PRINTS; PR00438; GFCYSKNOT.
DR ProDom; PD001629; -; 1.
DR PROSITE; PS00249; PDGF_1; 1.
DR PROSITE; PS0278; PDGF_2; 1.
DR SMART; SM00141; PDGF; 1.
KW Signal.
FT SIGNAL 1 31 POTENTIAL.
FT CHAIN 111 418 VASCULAR ENDOTHELIAL GROWTH FACTOR C.
SQ SEQUENCE 418 AA; 46839 MW; 099BFCC79151BF2B CRC64;

Query Match 12.1%; Score 89; DB 13; Length 418;
Best Local Similarity 18.0%; Pred. No. 0.072;
Matches 33; Conservative 20; Mismatches 56; Indels 74; Gaps 7;

QY 22 LDRLNDADAKRYSCTPRNSVNIIEEL-KLANVVFPRCLLVORCGGCG--CGTV-- 73
DB 118 LKSIDFWRKTCQMPREVCVDVKGKFGATTNTFFKPCVSIYRCGCCNSEGQCNMIST 177
QY 74 -----NWSCSTCNSKTV-KKYHEVLQ----- 94
DB 178 NVISKTLFEITVPLSHGPKPTVTSFANHTSCRCMSKLDVYRQVHSTIRRLSLPATQCHV 237
QY 95 ----PEPGHIKRRGRAKTMALVDIQLDHH-----ERDCDCICSS- 128
DB 238 ANKTCPKHVNWNQICRCLAQHDFGFGSHLGDSDTSEGPHICGNKELDEETCCQCKGG 297

Qy 129 -RP 130
||
Db 298 VRP 300

Search completed: September 26, 2001, 15:17:06
Job time: 117 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 26, 2001, 15:15:09 ; Search time 21.33 Seconds
(without alignments)
375,170 Million cell updates/sec

Title: US-09-662-783-4
Perfect score: 737
Sequence: 1 MYLTPYRGRSHYDRKSKV.....DIQLDHERCDCICSSRPPR 132

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 412676 seqs, 60623988 residues
Total number of hits satisfying chosen parameters: 412676

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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 - 22: /SID88/gcgdata/geneseq/geneseq/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	ID	Description
5 - 1	737	100.0	322	21	AAV71129 Human Platelet Der
2	737	100.0	370	21	AA848653 Human growth facto
3	737	100.0	370	21	AAV96864 SEQ. ID. 37 from W
4 - 4	737	100.0	370	21	AAV71130 Human Platelet Der
5	737	100.0	370	22	AA860888 Human VEGF-G prote
6	713	96.7	200	21	AAV71128 Human Platelet Der
7	686	93.1	370	21	AA848663 Mouse growth facto
8	681	92.4	370	22	AA860895 Human VEGF-G prote
9	380	51.6	66	21	AAV71132 Human Platelet Der
10	330	44.8	374	21	AA810639 Human VEGF-X prote
11	328.5	44.6	149	21	AA810642 Human VEGF-X PDGF-

12	328.5	44.6	318	21	AAV84558 A fragment of plat
13	328.5	44.6	339	21	AA858438 Lung cancer associ
14	328.5	44.6	345	20	AAV33679 Human VEGF-E prote
15	328.5	44.6	345	20	AAV41766 Human PRO200 prote
16	328.5	44.6	345	20	AAV30023 Human vascular end
17	328.5	44.6	345	21	AA848657 Human zvegfg3, SEQ
18	328.5	44.6	345	21	AA824250 Human platelet-der
19	328.5	44.6	345	21	AA844322 Human PRO200 (UNQ1
20	328.5	44.6	345	21	AA810633 Human RAGE generat
21	328.5	44.6	345	21	AA810634 Human VEGF-X homol
22	328.5	44.6	345	21	AA810635 Human VEGF-X prote
23	328.5	44.6	345	21	AA810636 Human VEGF-X prote
24	328.5	44.6	345	21	AA810644 Human VEGF-X prote
25	328.5	44.6	345	21	AA810650 Human 990126vegx p
26	328.5	44.6	345	21	AA810651 Human VEGF-X prote
27	328.5	44.6	345	21	AA819578 Human PRO200 (vasc
28	328.5	44.6	345	21	AA833414 Human PRO713 prote
29	328.5	44.6	345	21	AA824412 Human TANGO 128.
30	328.5	44.6	345	21	AA801419 Human growth facto
31	328.5	44.6	345	21	AA803003 Human growth facto
32	328.5	44.6	345	21	AAV96858 Amino acid sequenc
33	328.5	44.6	345	21	AAV84557 Bone morphogenic p
34	328.5	44.6	345	21	AAV59285 Human PRO200 prote
35	328.5	44.6	345	22	AA850980 Human PRO200 prote
36	328.5	44.6	345	22	AA849895 Human PRO200 prote
37	328.5	44.6	345	22	AA853074 Human angiogenesis
38	324.5	44.0	345	21	AA848658 Mouse zvegfg3, SEQ
39	324.5	44.0	345	21	AAV96861 Murine vascular en
40	324.5	44.0	345	21	AAV84559 A murine platelet-
41	318.5	43.2	354	21	AA810640 Human VEGF-X prote
42	318.5	43.2	354	21	AA810641 Human VEGF-X prote
43	308.5	41.9	113	21	AA810631 Human VEGF-X prote
44	308.5	41.9	113	21	AA810632 Human VEGF-X prote
45	292	39.6	227	21	AA810637 Human VEGF-X prote

ALIGNMENTS

RESULT 1
AAV71129
ID AAV71129 standard; peptide; 322 AA.
XX
AC AAV71129;
XX
DT 08-SEP-2000 (first entry)
XX
DE Human Platelet Derived Growth Factor (PDGF)-D partial polypeptide #2.
XX
KW Platelet Derived Growth Factor-D; PDGF-D; human; cytostatic; vulnerary;
KW VEGF-G; Vascular Endothelial Growth Factor; antithrombotic; tumour;
KW proliferative; activator; proliferation; differentiation; motility;
KW growth; PDGF-D receptor; antagonist; tissue remodelling; treat;
KW atherosclerosis; wound; metastasis.
XX
OS Homo sapiens.
XX
PW WO200027879-A1.
XX
PD 18-MAY-2000.
XX
PF 10-NOV-1999; 99WO-US26462.
XX
PR 10-NOV-1998; 98US-0107852.
PR 28-DEC-1998; 98US-0113997.
PR 28-AUG-1999; 99US-0150604.
PR 04-OCT-1999; 99US-0157108.
PR 05-OCT-1999; 99US-0157756.
XX
PA (LUDW-) LUDWIG INST CANCER RES.
PA (UYHE-) UNIV HELSINKI LICENSING LTD OY.
XX
PI Eriksson U, Aase K, Ponten A, Lee X, Uutela M, Alitalo K;

PI Oestman A, Heldin C;
 DR WPI; 2000-376495/32.
 DR N-PSDB; AAD00737.
 XX Novel polynucleotides encoding a novel growth factor of cells
 PT expressing a platelet-derived growth factor, useful for diagnostic and
 PT therapeutic applications, e.g. concerning cancer -
 XX
 XX
 PS Claim 25; Fig 6; 111pp; English.
 XX
 XX The present sequence is an N-terminally truncated polypeptide of human
 CC platelet derived growth factor (PDGF)-D, formally known as Vascular
 CC Endothelial Growth Factor (VEGF)-G. It is derived from human foetal lung
 CC lamda2g10 cDNA library. It belongs to the VEGF/PDGF family. It functions
 CC as an activator of proliferation, differentiation, growth and motility of
 CC cells, that express PDGF-D receptor. This sequence is useful for
 CC inhibiting the growth of tumours, that express PDGF-D. Expression of
 CC PDGF-D and its proteolytic cleavage for generating an activated truncated
 CC form is useful for regulating receptor binding specificity of PDGF-D.
 CC PDGF-D antagonist is useful for inhibiting tissue remodelling during the
 CC invasion of tumour cells into normal cells. PDGF-D may be used to treat
 CC wounds, atherosclerosis, metastasis and migration of smooth muscle cells.
 XX
 SQ Sequence 322 AA;

Query Match 100.0%; Score 737; DB 21; Length 322;
 Best Local Similarity 100.0%; Pred. No. 1.1e-73;
 Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MYLTPRYGRSYHDKRSKVDLRNDDAKRYSCPTPNYSVNIREEKLANVVFPRCLL 60
 Db 191 MYLTPRYGRSYHDKRSKVDLRNDDAKRYSCPTPNYSVNIREEKLANVVFPRCLL 250
 QY 61 VORCGNCGGVNWRSCNCGTKVKKYHEVLQFEPGHKRRGAKTALVDIQLDHHE 120
 Db 251 VQRCGNCGCGTVNWRSCNCGTKVKKYHEVLQFEPGHKRRGAKTALVDIQLDHHE 310
 QY 121 RDCICSSRPPR 132
 Db 311 RDCICSSRPPR 322

RESULT 2
 AAB48653
 ID AAB48653 standard; Protein; 370 AA.
 AC AAB48653;
 XX
 XX 09-MAR-2001 (first entry)
 XX Human growth factor homologue zveg4, SEQ ID NO:2.
 DE
 XX Human; zveg4; growth factor homologue; VEGF/PDGF family;
 KW CUB domain; PDGF-like activity; mitogenic; osteogenic;
 KW neovascularisation; tissue repair; proliferation; differentiation;
 KW liver damage; neurodegenerative; Alzheimer's disease; multiple sclerosis;
 KW periodontal disease; bone fracture; wound healing; vulnery; ischaemia;
 KW immunomodulation; hepatic; chromosome 11q22.3-23.1.
 XX
 OS Homo sapiens.
 XX
 PN WO200066736-A1.
 XX
 PD 09-NOV-2000.
 XX
 PF 03-MAY-2000; 2000WO-US40047.
 XX
 PR 03-MAY-1999; 99US-0304216.
 PR 10-NOV-1999; 99US-0164463.
 PR 04-FEB-2000; 2000US-0180169.
 XX

PA (ZYMO) ZYMOGENETICS INC.
 XX Gilbert T, Hart CE, Sheppard PO, Gilbertson DG;
 XX WPI: 2000-687541/67,
 DR N-PSDB; AAC81555.
 XX Growth factor homologs and the nucleic acids that encode them, useful
 PT e.g. for treating liver damage, ischemia, multiple sclerosis and
 PT Alzheimer's disease -
 XX
 XX Claim 1; Page 110-111; 143pp; English.
 PS
 XX The invention relates to the human growth factor homologue zveg4
 CC (AAB48653), and nucleic acids encoding it (AAC81555). zveg4 is a member
 CC of the PDGF (platelet-derived growth factor)/VEGF (vascular endothelial
 CC growth factor) family. zveg4 has a growth factor domain (AAB48654)
 CC characterised by a PDGF cysteine knot structure, and a CUB domain
 CC (AAB48655) which has a beta barrel structure. zveg4 has PDGF-like
 CC activity, having mitogenic activity on fibroblasts, vascular smooth
 CC muscle cells and pericytes, and has also been shown to stimulate bone
 CC growth. The invention also relates to fusion proteins comprising human
 CC zveg4 or fragments thereof, particularly human zveg4/human zveg3
 CC fusions; expression constructs and host cells comprising human zveg4
 CC nucleic acids; the recombinant expression of human zveg4; an antibody
 CC which binds to human zveg4 or a fragment thereof; a method of activating
 CC a cell-surface PDGF receptor using a zveg4-derived polypeptide; a
 CC method of modulating the proliferation, differentiation, migration or
 CC metabolism of bone cells, comprising exposing bone cells to
 CC zveg4-derived polypeptides; and a method of detecting a genetic
 CC abnormality in the zveg4 gene of a patient. zveg4 proteins and derived
 CC fragments may be used to stimulate tissue development or repair, or
 CC cellular differentiation or proliferation. They are particularly used for
 CC the treatment or repair of liver damage, and may also be used to
 CC modulate neurite growth (e.g., in the treatment of Alzheimer's disease or
 CC multiple sclerosis). Due to their osteogenic activity, they may be used
 CC in the treatment of periodontal disease and fractures. They may also be
 CC used to enhance expansion and mobilisation of haematopoietic stem cells
 CC and endothelial precursor stem cells, which may be useful in the
 CC treatment of ischaemia, in wound healing, and in the modulation of the
 CC immune system. The present sequence represents human zveg4.
 XX
 SQ Sequence 370 AA;

Query Match 100.0%; Score 737; DB 21; Length 370;
 Best Local Similarity 100.0%; Pred. No. 1.3e-73;
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 Db 239 MYLTPRYGRSYHDKRSKVDLRNDDAKRYSCPTPNYSVNIREEKLANVVFPRCLL 298
 QY 61 VORCGNCGGVNWRSCNCGTKVKKYHEVLQFEPGHKRRGAKTALVDIQLDHHE 120
 Db 299 VQRCGNCGCGTVNWRSCNCGTKVKKYHEVLQFEPGHKRRGAKTALVDIQLDHHE 358
 QY 121 RDCICSSRPPR 132
 Db 359 RDCICSSRPPR 370

RESULT 3
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 ID AAY96864 standard; Protein; 370 AA.
 XX
 XX AAY96864;
 XX
 XX 26-SEP-2000 (first entry)
 XX
 DE SEQ. ID. 37 from WO0034474.
 XX
 KW Vascular endothelial growth factor; homologue; zveg3; CUB domain;


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seq_documentation_block:
LOCUS      AA488780          360 bp      mRNA          EST          15-AUG-1997
DEFINITION aa54c10.r1.nci CGAP_GCB1 Homo sapiens CDNA clone IMAGE:824754 5',
            mRNA sequence.
ACCESSION  AA488780
VERSION    AA488780.1 GI:2218382
SOURCE     human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
            1 (bases 1 to 360)
REFERENCE  NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
AUTHORS   National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
TITLE     Tumor Gene Index
JOURNAL    Unpublished (1997)
COMMENT    Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-re@mail.nih.gov
            Tissue Procurement: Louis M. Staudt, M.D., David Allman,
            Ph.D., Gerald Marti, M.D.
            CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
            Bonaldo, Ph.D.
            CDNA Library Arrayed by: Greg Lennon, Ph.D.
            DNA Sequencing by: Washington University Genome Sequencing Center
            Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/obrp/image/image.html
            Seq primer: -28ml3 rev1 ET from Amersham
            High quality sequence stop: 358.
FEATURES             Location/Qualifiers
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                     /tissue_type="germinal center B cell"
                     /lab_host="DH10B"
                     /note="Vector: pT73D-Pac (Pharmacia) with a modified
                     polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
                     was prepared from human tonsillar cells enriched for
                     germinal center B cells by flow sorting (CD20+, IgD-),
                     provided by Dr. Louis M. Staudt (NCI). Dr. David Allman
                     (NCI) and Dr. Gerald Marti (CEBR). CDNA synthesis was
                     primed with a Not I - oligo(dT) primer
                     [5'-TGTACCAATCTGAAGTGGAGCGCGCCCTCATTTTCTTTTCTTTT-3'
                     ]. Double-stranded cDNA was ligated to Eco RI adaptors
                     (Pharmacia), digested with Not I and cloned into the Not I
                     and Eco RI sites of the modified pT73 vector. Library
                     went through one round of normalization, and was
                     constructed by Bento Soares and M. Fatima Bonaldo."
BASE COUNT      108 a      77 c      86 g      89 t

alignment_scores:
  Quality: 380.00      Length: 360
  Ratio: 5.758        Gaps: 0
  Percent Similarity: 100.000      Percent Identity: 100.000

alignment_block:
US-09-662-783-4 x AA488780

Align seg 1/1 to: AA488780 from: 1 to: 360

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|||||
83 yLysThrValLysLysThrHisGluValLeuGlnPheGluProGlyHis1 100
|||||
51 GAAACCGTGAAAGATATCATGAGTATTACAGTTTGAGCTGCGCCACA 100
|||||
100 LeLysArgArgGlyArgAlaLysThrMetAlaLeuValAspIleGlnLeu 116
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|||||
101 TCAAGAGGAGGGGTAGAGCTAAGACCATGCTCTAGTTGACATCCAGTTG 150
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117 AspHisHisGluArgCysAspCysIleCysSerSerArgProProArg 132
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151 GATCACCATGAACGATGTGATTGTATCTGCGAGCTCAAGACCATCGA 198
|||||
seq_name: gb_est82:BF021679

seq_documentation_block:
LOCUS      BF021679          523 bp      mRNA          EST          29-DEC-2000
DEFINITION uy50f05.y1 NCI_CGAP_Lu30 Mus musculus cDNA clone IMAGE:3663009 5',
            similar to TR:Q90Y71 Q90Y71 FALLOTEIN.; mRNA sequence.
ACCESSION  BF021679
VERSION    BF021679.1 GI:10753011
KEYWORDS   EST.
SOURCE     house mouse.
ORGANISM   Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
            1 (bases 1 to 523)
REFERENCE  NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
AUTHORS   National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
TITLE     Tumor Gene Index
JOURNAL    Unpublished (1997)
COMMENT    Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-re@mail.nih.gov
            Tissue Procurement: Gilbert Smith, Ph.D.
            CDNA Library Preparation: Life Technologies, Inc.
            CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Washington University Genome Sequencing Center
            Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            image.llnl.gov/image/html/iresources.shtml
            MGI:1423777
            Seq primer: -40RP from Gibco
            High quality sequence stop: 452.
FEATURES             Location/Qualifiers
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                     /clone="IMAGE:3663009"
                     /clone_lib="NCI_CGAP_Lu30"
                     /tissue_type="tumor, metastatic to mammary"
                     /lab_host="DH10B"
                     /note="Organ: lung; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; transgenic model WNT-1, expression driven by
                     MMTV-LTR enhancer; Cloned unidirectionally. Primer: Oligo
                     dt. Library constructed by Life Technologies."
BASE COUNT      143 a      116 c      139 g      125 t

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alignment_block:
US-09-662-783-4 x BF021679

Align seg 1/1 to: BF021679 from: 1 to: 523

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|||||
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|||||
16 glySerLys...ValAspLeuAspArgLeuAsnAspAspAlaLysArgT 32
|||||
181 AAAAGCAAGTGGTGAATCTGAATCTCTCTAAAGGAAGAGGTAACACT 230
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